

SEQUENCE LISTING

<110> Bejanin, Stephane
Tanaka, Hiroaki

<120> HUMAN CDNAS AND PROTEINS AND USES THEREOF

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<141> 2001-08-06

<150> US 60/305,456

<151> 2001-07-13

<150> US 60/302,277

<151> 2001-06-29

<150> US 60/298,698

<151> 2001-06-15

<150> US 60/293,574

<151> 2001-05-25

<160> 112

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Phe Ser Cys Leu Pro Arg Pro Arg Thr Glu Pro Leu Val Ala Ser Thr
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gac cac acc aaa atg cca tct caa atg gaa cac gcc atg gaa acc atg 1581
Asp His Thr Lys Met Pro Ser Gln Met Glu His Ala Met Glu Thr Met
35 40 45
atg ttt aca ttt cac aaa ttc gct ggg gat aaa ggc tac tta aca aag 1629
Met Phe Thr Phe His Lys Phe Ala Gly Asp Lys Gly Tyr Leu Thr Lys
50 55 60 65
gag gac ctg aga gta ctc atg gaa aag gag ttc cct gga ttt ttg gaa 1677
Glu Asp Leu Arg Val Leu Met Glu Lys Glu Phe Pro Gly Phe Leu Glu
70 75 80
aat caa aaa gac cct ctg gct gtg gac aaa ata atg aag gac ctg gac 1725
Asn Gln Lys Asp Pro Leu Ala Val Asp Lys Ile Met Lys Asp Leu Asp
85 90 95
cag tgt aga gat ggc aaa gtg ggc ttc cag agc ttc ttt tcc cta att 1773
Gln Cys Arg Asp Gly Lys Val Gly Phe Gln Ser Phe Phe Ser Leu Ile
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Ala Gly Leu Thr Ile Ala Cys Asn Asp Tyr Phe Val Val His Met Lys
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Gln Lys Gly Lys Lys
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Lys Glu Asp Leu Arg Val Leu Met Glu Lys Glu Phe Pro Gly Phe Leu
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 Ser Tyr Gly Gly Lys Met Ala Ala Gly Ile Gly Leu Glu Leu Tyr Lys
 145 150 155
 gcc att cag cga ggg acc atc aag tgc aac ttt gcg ggg gtt gcc ttg 632
 Ala Ile Gln Arg Gly Thr Ile Lys Cys Asn Phe Ala Gly Val Ala Leu
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 Gly Asp Ser Trp Ile Ser Pro Val Asp Ser Val Leu Ser Trp Gly Pro
 175 180 185
 tac ctg tac agc atg tct ctt ctc gaa gac aaa ggt ctg gca gag gtg 728
 Tyr Leu Tyr Ser Met Ser Leu Leu Glu Asp Lys Gly Leu Ala Glu Val
 190 195 200 205
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 Ser Lys Val Ala Glu Gln Val Leu Asn Ala Val Asn Lys Gly Leu Tyr
 210 215 220
 aga gag gcc aca gag ctg tgg ggg aaa gca gaa atg atc att gaa cag 824
 Arg Glu Ala Thr Glu Leu Trp Gly Lys Ala Glu Met Ile Ile Glu Gln
 225 230 235
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 Val Lys Arg Gly Asn Thr Gln Arg Leu Ala Cys Leu Ala Phe Ser Gly
 240 245 250
 ggg tac agg gcc cat ggt tgg tgt tgt caa act tgg agt cta cac 917
 Gly Tyr Arg Ala His Gly Trp Cys Cys Gln Thr Trp Ser Leu His
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 40 45 50
 Ser Ser Thr Gly Phe Gly Asn Phe Glu Glu Ile Gly Pro Leu Asp Ser
 55 60 65 70
 Asp Leu Lys Pro Arg Lys Thr Thr Trp Leu Gln Ala Ala Ser Leu Leu
 75 80 85
 Phe Val Asp Asn Pro Val Gly Thr Gly Phe Ser Tyr Val Asn Gly Ser
 90 95 100
 Gly Ala Tyr Ala Lys Asp Leu Ala Met Val Ala Ser Asp Met Met Val
 105 110 115
 Leu Leu Lys Thr Phe Phe Ser Cys His Lys Glu Phe Gln Thr Val Pro
 120 125 130

Phe Tyr Ile Phe Ser Glu Ser Tyr Gly Gly Lys Met Ala Ala Gly Ile
 135 140 145 150
 Gly Leu Glu Leu Tyr Lys Ala Ile Gln Arg Gly Thr Ile Lys Cys Asn
 155 160 165
 Phe Ala Gly Val Ala Leu Gly Asp Ser Trp Ile Ser Pro Val Asp Ser
 170 175 180
 Val Leu Ser Trp Gly Pro Tyr Leu Tyr Ser Met Ser Leu Leu Glu Asp
 185 190 195
 Lys Gly Leu Ala Glu Val Ser Lys Val Ala Glu Gln Val Leu Asn Ala
 200 205 210
 Val Asn Lys Gly Leu Tyr Arg Glu Ala Thr Glu Leu Trp Gly Lys Ala
 215 220 225 230
 Glu Met Ile Ile Glu Gln Val Lys Arg Gly Asn Thr Gln Arg Leu Ala
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 Ala Leu Met Ile Ser Met Ile Ser Ala Asp Ser His Glu Lys Arg His
 -5 1 5
 cat ggg tat aga aga aaa ttc cat gaa aag cat cat tca tac cat atc 209
 His Gly Tyr Arg Arg Lys Phe His Glu Lys His His Ser Tyr His Ile
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 aca cta cta cca ctt ttt gaa gaa tca tca aag agc aat gca aat gaa 257
 Thr Leu Leu Pro Leu Phe Glu Glu Ser Ser Lys Ser Asn Ala Asn Glu
 25 30 35 40
 aaa cac tat aat tta ctg tat act ctt tgt ttc agg ata ctt gcc ttt 305
 Lys His Tyr Asn Leu Leu Tyr Thr Leu Cys Phe Arg Ile Leu Ala Phe
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 tca att gtc act tgatgatata attgcaattt aaactgttaa gctgtgttca 357
 Ser Ile Val Thr

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Phe His Glu Lys His His Ser Tyr His Ile Thr Leu Leu Pro Leu Phe
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Met Thr Gln Ser Pro Leu Phe Leu Pro Val Thr Pro Gly Glu Pro Ala
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Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Val Gln Gly Ser
25 30 35

aac tat ttg gat tgg tac cac cag aag cca ggg cag tct cca caa ctc 244
 Asn Tyr Leu Asp Trp Tyr His Gln Lys Pro Gly Gln Ser Pro Gln Leu
 40 45 50
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 Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe
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 Pro Phe Thr Phe Gly Pro Gly Thr Arg Val Asp Ile Lys Arg Thr Val
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 Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys
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 Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg
 135 140 145
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 Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn
 150 155 160
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 Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser
 165 170 175 180
 ctc agc agc acc ctg acg ctg agc aaa gca gac tac gag aaa cac aaa 676
 Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys
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 Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala
 45 50 55 60
 Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
 65 70 75

Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
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 Cys Met Gln Ala Leu Gln Thr Pro Phe Thr Phe Gly Pro Gly Thr Arg
 95 100 105
 Val Asp Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
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 Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
 125 130 135 140
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 145 150 155
 Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
 160 165 170
 Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
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 Met Ser Ala Ser Cys Cys Leu Ser Trp Cys Pro Ala
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 Lys Ala Lys Ser Lys Cys Gly Pro Thr Phe Phe Pro Cys Ala Ser Gly
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 Ile His Cys Ile Ile Gly Arg Phe Arg Cys Asn Gly Phe Glu Asp Cys
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 Pro Asp Gly Ser Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys
 35 40 45
 tcc acc gcc cgc tac cac tgc aag aac ggc ctc tgt att gac aag agc 481
 Ser Thr Ala Arg Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser
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 Phe Ile Cys Asp Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu
 65 70 75
 agc tgt gaa agt tct caa gct att ttt cca caa att act gtg tcc 574
 Ser Cys Glu Ser Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser
 80 85 90
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 Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys Ser Thr Ala Arg
 35 40 45 50
 Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser Phe Ile Cys Asp
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 Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Ser Cys Glu Ser
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 Ile His Cys Ile Ile Gly Arg Phe Arg Cys Asn Gly Phe Glu Asp Cys
 20 25 30
 ccc gat ggc agc gat gaa gag aac tgc aca gca aac cct ctg ctt tgc 433
 Pro Asp Gly Ser Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys
 35 40 45
 tcc acc gcc cgc tac cac tgc aag aac ggc ctc tgt att gac aag agc 481

Ser Thr Ala Arg Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser
 50 55 60
 ttc atc tgc gat gga cag aat aac tgt caa gac aac agt gat gag gaa 529
 Phe Ile Cys Asp Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu
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 agc tgt gaa agt tct caa gct att ttt cca caa att act gtg tcc 574
 Ser Cys Glu Ser Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser
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 35 40 45 50
 Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser Phe Ile Cys Asp
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 gattaatcca tgggcaggcc tggaaaaagt cccactccag tctgcgggac ccacagcctg 180
 gccctcaggc ctcaggcctt cctctggcttg aagattgggc ttcacctggg acctaccctt 240
 tctgcttagg agc atg tct gcc tcc tgc tgc ctt tca tgg tgc cca gcc 289
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Ile His Cys Ile Ile Gly Arg Phe Arg Cys Asn Gly Phe Glu Asp Cys
          20          25          30
ccc gat ggc agc gat gaa gag aac tgc aca gca aac cct ctg ctt tgc 433
Pro Asp Gly Ser Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys
          35          40          45
ttc acc gcc cgc tac cac tgc aag aac ggc ctc tgt att gac aag agc 481
Ser Thr Ala Arg Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser
          50          55          60
ttc atc tgc gat gga cag aat aac tgt caa gac aac agt gat gag gaa 529
Phe Ile Cys Asp Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu
          65          70          75
agc tgt gaa agt tct caa gct att ttt cca caa att act gtg tcc 574
Ser Cys Glu Ser Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser
          80          85          90
tgagccctga gctaattaag tgctggataa gcatcacctc ccagtaatcc tgttatcagc 634
ctttgaaatg taggtagctt attatccaca ttttgcagat gaggaacacag agtcagggtga 694
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Ile Gly Arg Phe Arg Cys Asn Gly Phe Glu Asp Cys Pro Asp Gly Ser
          20          25          30
Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys Ser Thr Ala Arg
          35          40          45          50
Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser Phe Ile Cys Asp
          55          60          65
Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu Ser Cys Glu Ser
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Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser
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 gattaatcca tgggcaggcc tggaaaagtt cccactccag tctgcgggac ccacagcctg 180
 gccctcagggc ytcaggcctt cccaggccttg aagattgggc ttcacctggg acctaccctt 240
 tctgcctagg agc atg tct gcc tcc tgc tgc ctt tca tgg tgc cca gcc 289

Met Ser Ala Ser Cys Cys Leu Ser Trp Cys Pro Ala

-10

-5

aag gct aag tgc aaa tgt ggc cca acc ttc ttc ccc tgt gcc agc ggc 337
 Lys Ala Lys Ser Lys Cys Gly Pro Thr Phe Phe Pro Cys Ala Ser Gly

1

5

10

atc cat tgc atc att ggt cgc ttc cgg tgc aat ggg ttt gag gac tgt 385
 Ile His Cys Ile Ile Gly Arg Phe Arg Cys Asn Gly Phe Glu Asp Cys

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25

30

ccc gat ggc agc gat gaa gag aac tgc aca gca aac cct ctg ctt tgc 433
 Pro Asp Gly Ser Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys

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40

45

tcc acc gcc cgc tac cac tgc aag aac ggc ctc tgt att gac aag agc 481
 Ser Thr Ala Arg Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser

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55

60

ttc atc tgc gat gga cag aat aac tgt caa gac aac agt gat gag gaa 529
 Phe Ile Cys Asp Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Gly Glu

65

70

75

agc tgt gaa agt tct caa gct att ttt cca caa att act gtg tcc 574
 Ser Cys Glu Ser Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser

80

85

90

tgagccctga gctaattaag tgctggataa gcatcacctc ccagtaatcc tggttatcagc 634
 ctttgaaatg taggtagctt tattatccac attttgcaga tgaggaaaca gagtccaggtg 694
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-10

-5

1

Lys Cys Gly Pro Thr Phe Phe Pro Cys Ala Ser Gly Ile His Cys Ile

5

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15

Ile Gly Arg Phe Arg Cys Asn Gly Phe Glu Asp Cys Pro Asp Gly Ser

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25

30

Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys Ser Thr Ala Arg

35

40

45

50

Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser Phe Ile Cys Asp

55

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Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu Ser Cys Glu Ser

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Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser

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aaccctctgc agcaagacgt ggtgatggca attggtggaa aggagaaaat cacagaggaa 180
taggaactttt cccatccaat ttgtaacaa ctaatttaaa catagagact gaggcagcgcg 240
ctgtggacaa attgaatgta attgatgatg atgtggagga aattaagaaa tcagagcctg 300
agcctgttta tatagatgag gataag atg gat aga gcc ctg cag gta ctt cag 353
                               Met Asp Arg Ala Leu Gln Val Leu Gln
                               1           5
agt ata gat cca aca gat tca aaa cca gac tcc caa gac ctt ttg gat 401
Ser Ile Asp Pro Thr Asp Ser Ser Lys Pro Asp Ser Gln Asp Leu Leu Asp
10                               15           20           25
tta gaa gat atc tgc caa cag atg ggt cca atg ata gat gaa aaa ctt 449
Leu Glu Asp Ile Cys Gln Gln Met Gly Pro Met Ile Asp Glu Lys Leu
30                               35           40
gaa gaa att gat agg aag cat tca gaa ttg tct gaa ttg aat gtt aaa 497
Glu Glu Ile Asp Arg Lys His Ser Glu Leu Ser Glu Leu Asn Val Lys
45                               50           55
gtc ctg gaa gct ctg gaa cta tat aac aaa ttg gtg aat gaa gca cca 545
Val Leu Glu Ala Leu Glu Leu Tyr Asn Lys Leu Val Asn Glu Ala Pro
60                               65           70
gtg tac tca gtc tat tca aag ctc cac cct cca gca cat tac cca cct 593
Val Tyr Ser Val Tyr Ser Lys Leu His Pro Pro Ala His Tyr Pro Pro
75                               80           85
gca tca tct ggg gtt cca atg cag aca tat cca gtt caa tca cat ggt 641
Ala Ser Ser Gly Val Pro Met Gln Thr Tyr Pro Val Gln Ser His Gly
90                               95           100           105
gga aac tat atg ggt cag agc att cac caa gta act gtt gcc caa agc 689
Gly Asn Tyr Met Gly Gln Ser Ile His Gln Val Thr Val Ala Gln Ser
110                               115           120
tat agc cta gga ccc gat caa att ggt cca ctg aga tct ctg cct cca 737
Tyr Ser Leu Gly Pro Asp Gln Ile Gly Pro Leu Arg Ser Leu Pro Pro
125                               130           135
aat gtg aat tcc tca gtg aca gca cag cct gct caa act tca tat tta 785
Asn Val Asn Ser Ser Val Thr Ala Gln Pro Ala Gln Thr Ser Tyr Leu
140                               145           150
agc act gga caa gac act gtt tcc aat cct act tat atg aac cag aac 833
Ser Thr Gly Gln Asp Thr Val Ser Asn Pro Thr Tyr Met Asn Gln Asn
155                               160           165
tct aac cta cag tca gct act ggt aca act gct tac aca cag caa atg 881
Ser Asn Leu Gln Ser Ser Ala Thr Gly Thr Ala Tyr Thr Gln Gln Met
170                               175           180           185
ggg atg tct gtg gat atg tca tct tat cag aac act act tcc aat ttg 929
Gly Met Ser Val Asp Met Ser Ser Tyr Gln Asn Thr Thr Ser Asn Leu
190                               195           200
cct caa ctg gca ggc ttt ccg gtg aca gtt cca gct cat cca gtt gca 977

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Pro Gln Leu Ala Gly Phe Pro Val Thr Val Pro Ala His Pro Val Ala
 205 210 215
 cag cag cac aca aat tac cat cag cag cct ctc ctt tagaacaaca 1023
 Gln Gln His Thr Asn Tyr His Gln Gln Pro Leu Leu
 220 225
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 aaaatattaa aacttttttc cctctcaact caaaaggacc atgaataaat aaagcaca 1143
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 <213> Homo sapiens

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 35 40 45
 Ser Glu Leu Ser Glu Leu Asn Val Lys Val Leu Glu Ala Leu Glu Leu
 50 55 60
 Tyr Asn Lys Leu Val Asn Glu Ala Pro Val Tyr Ser Val Tyr Ser Lys
 65 70 75 80
 Leu His Pro Pro Ala His Tyr Pro Pro Ala Ser Ser Gly Val Pro Met
 85 90 95
 Gln Thr Tyr Pro Val Gln Ser His Gly Gly Asn Tyr Met Gly Gln Ser
 100 105 110
 Ile His Gln Val Thr Val Ala Gln Ser Tyr Ser Leu Gly Pro Asp Gln
 115 120 125
 Ile Gly Pro Leu Arg Ser Leu Pro Pro Asn Val Asn Ser Ser Val Thr
 130 135 140
 Ala Gln Pro Ala Gln Thr Ser Tyr Leu Ser Thr Gly Gln Asp Thr Val
 145 150 155 160
 Ser Asn Pro Thr Tyr Met Asn Gln Asn Ser Asn Leu Gln Ser Ala Thr
 165 170 175
 Gly Thr Thr Ala Tyr Thr Gln Gln Met Gly Met Ser Val Asp Met Ser
 180 185 190
 Ser Tyr Gln Asn Thr Thr Ser Asn Leu Pro Gln Leu Ala Gly Phe Pro
 195 200 205
 Val Thr Val Pro Ala His Pro Val Ala Gln Gln His Thr Asn Tyr His
 210 215 220
 Gln Gln Pro Leu Leu
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 Met Arg
 -15
 gcc tgg atc ttc ttt ctc ctt tgc ctg gcc ggg agg gcc ttg gca gcc 165
 Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala Leu Ala Ala
 -10 -5 1
 cct cag caa gaa gcc ctg cct gat gag aca gag gtg gtg gaa gaa act 213
 Pro Gln Gln Glu Ala Leu Pro Asp Glu Thr Glu Val Val Glu Glu Thr
 5 10 15
 gtg gca gag gtg act gag gta tct gtt gga gct aat cct gtc cag gtg 261
 Val Ala Glu Val Thr Glu Val Ser Val Gly Ala Asn Pro Val Gln Val
 20 25 30
 gaa gta gga gaa ttt gat gat ggt gca gag gaa acc gaa gag gag gtg 309
 Glu Val Gly Glu Phe Asp Asp Gly Ala Glu Glu Thr Glu Glu Glu Val
 35 40 45 50
 gtg gcg gaa aat ccc tgc cag aac cac cac tgc aaa cac gcc aag gtg 357
 Val Ala Glu Asn Pro Cys Gln Asn His His Cys Lys His Gly Lys Val
 55 60 65
 tgc gag ctg gat gag aac aac acc ccc atg tgc gtg tgc cag gac ccc 405
 Cys Glu Leu Asp Glu Asn Asn Thr Pro Met Cys Val Cys Gln Asp Pro
 70 75 80
 acc agc tgc cca gcc ccc att ggc gag ttt gag aag gtg tgc agc aat 453
 Thr Ser Cys Pro Ala Pro Ile Gly Glu Phe Glu Lys Val Cys Ser Asn
 85 90 95
 gac aac aag acc ttc gac tct tcc tgc cac ttc ttt gcc aca aag tgc 501
 Asp Asn Lys Thr Phe Asp Ser Ser Cys His Phe Phe Ala Thr Lys Cys
 100 105 110
 acc ctg gag ggc acc aag aag ggc cac aag ctc cac ctg gac tac atc 549
 Thr Leu Glu Gly Thr Lys Lys Gly His Lys Leu His Leu Asp Tyr Ile
 115 120 125 130
 ggg cct tgc aaa tac atc ccc cct tgc ctg gac tct gag ctg acc gaa 597
 Gly Pro Cys Lys Tyr Ile Pro Pro Cys Leu Asp Ser Glu Leu Thr Glu
 135 140 145
 ttc ccc ctg cgc atg cgg gac tgg ctc aag aac gtc ctg gtc acc ctg 645
 Phe Pro Leu Arg Met Arg Asp Trp Leu Lys Asn Val Leu Val Thr Leu
 150 155 160
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 Tyr Glu Arg Asp Glu Asp Asn Asn Leu Leu Thr Glu Lys Gln Lys Leu
 165 170 175
 cgg gtg aag aag atc cat gag aat gag aag cgc ctg gag gca gga gac 741
 Arg Val Lys Lys Ile His Glu Asn Glu Lys Arg Leu Glu Ala Gly Asp
 180 185 190
 cac ccc gtg gag ctg ctg gcc cgg gac tgc cag gct gtt tca gcc agg 789
 His Pro Val Glu Leu Leu Ala Arg Asp Cys Gln Ala Val Ser Ala Arg
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 20 25 30
 Gln Val Glu Val Gly Glu Phe Asp Asp Gly Ala Glu Glu Thr Glu Glu
 35 40 45
 Glu Val Val Ala Glu Asn Pro Cys Gln Asn His His Cys Lys His Gly
 50 55 60
 Lys Val Cys Glu Leu Asp Glu Asn Asn Thr Pro Met Cys Val Cys Gln
 65 70 75
 Asp Pro Thr Ser Cys Pro Ala Pro Ile Gly Glu Phe Glu Lys Val Cys
 80 85 90 95
 Ser Asn Asp Asn Lys Thr Phe Asp Ser Ser Cys His Phe Phe Ala Thr
 100 105 110
 Lys Cys Thr Leu Glu Gly Thr Lys Lys Gly His Lys Leu His Leu Asp
 115 120 125
 Tyr Ile Gly Pro Cys Lys Tyr Ile Pro Pro Cys Leu Asp Ser Glu Leu
 130 135 140
 Thr Glu Phe Pro Leu Arg Met Arg Asp Trp Leu Lys Asn Val Leu Val
 145 150 155
 Thr Leu Tyr Glu Arg Asp Glu Asp Asn Asn Leu Leu Thr Glu Lys Gln
 160 165 170 175
 Lys Leu Arg Val Lys Lys Ile His Glu Asn Glu Lys Arg Leu Glu Ala
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 gctaaa atg aag act ctg cag tct aca ctt ctc ctg tta ctg ctt gtg 168
 Met Lys Thr Leu Gln Ser Thr Leu Leu Leu Leu Leu Val
 -15 -10 -5
 cct ctg ata aag cca gca cca cca acc cag cag gac tca cgc att atc 216
 Pro Leu Ile Lys Pro Ala Pro Pro Thr Gln Gln Asp Ser Arg Ile Ile
 1 5 10
 tat gat tat gga aca gat aat ttt gaa gaa tcc ata ttt agc caa gat 264
 Tyr Asp Tyr Gly Thr Asp Asn Phe Glu Glu Ser Ile Phe Ser Gln Asp
 15 20 25
 tat gag gat aaa tac ctg gat gga aaa aat att aag gaa aaa gaa act 312
 Tyr Glu Asp Lys Tyr Leu Asp Gly Lys Asn Ile Lys Glu Lys Glu Thr
 30 35 40
 gtg ata ata ccc aat gag aaa agt ctt caa tta caa aaa gat gag gca 360

Val	Ile	Ile	Pro	Asn	Glu	Lys	Ser	Leu	Gln	Leu	Gln	Lys	Asp	Glu	Ala	
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ata	aca	cca	tta	cct	ccc	aag	aaa	gaa	aat	gat	gaa	atg	ccc	acg	tgt	408
Ile	Thr	Pro	Leu	Pro	Pro	Lys	Lys	Glu	Asn	Asp	Glu	Met	Pro	Thr	Cys	
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ctg	ctg	tgt	gtt	tgt	tta	agt	ggc	tct	gta	tac	tgt	gaa	gaa	gtt	gac	456
Leu	Leu	Cys	Val	Cys	Leu	Ser	Gly	Ser	Val	Tyr	Cys	Glu	Glu	Val	Asp	
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att	gat	gct	gta	cca	ccc	tta	cca	aag	gaa	tca	gcc	tat	ctt	tac	gca	504
Ile	Asp	Ala	Val	Pro	Pro	Leu	Pro	Lys	Glu	Ser	Ala	Tyr	Leu	Tyr	Ala	
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cga	ttc	aac	aaa	att	aaa	aag	ctg	act	gcc	aaa	gat	ttt	gca	gac	ata	552
Arg	Phe	Asn	Lys	Ile	Lys	Lys	Leu	Thr	Ala	Lys	Asp	Phe	Ala	Asp	Ile	
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Pro	Asn	Leu	Arg	Arg	Leu	Asp	Phe	Thr	Gly	Asn	Leu	Ile	Glu	Asp	Ile	
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Glu	Asp	Gly	Thr	Phe	Ser	Lys	Leu	Ser	Leu	Leu	Glu	Glu	Leu	Ser	Leu	
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Ala	Glu	Asn	Gln	Leu	Lys	Leu	Pro	Pro	Val	Leu	Pro	Pro	Lys	Leu	Thr	
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Leu	Phe	Asn	Ala	Lys	Tyr	Asn	Lys	Ile	Lys	Ser	Arg	Gly	Ile	Lys	Ala	
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Asn	Ala	Phe	Lys	Lys	Leu	Asn	Asn	Leu	Thr	Phe	Leu	Tyr	Leu	Asp	His	
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aat	gcc	ctg	gaa	tcc	gtg	cct	ctt	aat	tta	cca	gaa	agt	cta	cgt	gta	840
Asn	Ala	Leu	Glu	Ser	Val	Pro	Lys	Asn	Leu	Pro	Glu	Ser	Leu	Arg	Val	
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Ile	His	Leu	Gln	Phe	Asn	Asn	Ile	Ala	Ser	Ile	Thr	Asp	Asp	Thr	Phe	
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tgc	aag	gct	aat	gac	acc	agt	tac	atc	cgg	gac	cgc	att	gaa	gag	ata	936
Cys	Lys	Ala	Asn	Asp	Thr	Ser	Tyr	Ile	Arg	Asp	Arg	Ile	Glu	Glu	Ile	
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cgc	ctg	gag	ggc	aat	cca	atc	gtc	ctg	gga	aag	cat	cca	aac	agt	ttt	984
Arg	Leu	Glu	Gly	Asn	Pro	Ile	Val	Leu	Gly	Lys	His	Pro	Asn	Ser	Phe	
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Ile	Cys	Leu	Lys	Arg	Leu	Pro	Ile	Gly	Ser	Tyr	Phe					
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 Tyr Gly Thr Asp Asn Phe Glu Glu Ser Ile Phe Ser Gln Asp Tyr Glu
 15 20 25
 Asp Lys Tyr Leu Asp Gly Lys Asn Ile Lys Glu Lys Glu Thr Val Ile
 30 35 40 45
 Ile Pro Asn Glu Lys Ser Leu Gln Leu Gln Lys Asp Glu Ala Ile Thr
 50 55 60
 Pro Leu Pro Pro Lys Lys Glu Asn Asp Glu Met Pro Thr Cys Leu Leu
 65 70 75
 Cys Val Cys Leu Ser Gly Ser Val Tyr Cys Glu Glu Val Asp Ile Asp
 80 85 90
 Ala Val Pro Pro Leu Pro Lys Glu Ser Ala Tyr Leu Tyr Ala Arg Phe
 95 100 105
 Asn Lys Ile Lys Lys Leu Thr Ala Lys Asp Phe Ala Asp Ile Pro Asn
 110 115 120 125
 Leu Arg Arg Leu Asp Phe Thr Gly Asn Leu Ile Glu Asp Ile Glu Asp
 130 135 140
 Gly Thr Phe Ser Lys Leu Ser Leu Leu Glu Glu Leu Ser Leu Ala Glu
 145 150 155
 Asn Gln Leu Leu Lys Leu Pro Val Leu Pro Pro Lys Leu Thr Leu Phe
 160 165 170
 Asn Ala Lys Tyr Asn Lys Ile Lys Ser Arg Gly Ile Lys Ala Asn Ala
 175 180 185
 Phe Lys Lys Leu Asn Asn Leu Thr Phe Leu Tyr Leu Asp His Asn Ala
 190 195 200 205
 Leu Glu Ser Val Pro Leu Asn Leu Pro Glu Ser Leu Arg Val Ile His
 210 215 220
 Leu Gln Phe Asn Asn Ile Ala Ser Ile Thr Asp Asp Thr Phe Cys Lys
 225 230 235
 Ala Asn Asp Thr Ser Tyr Ile Arg Asp Arg Ile Glu Glu Ile Arg Leu
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 Glu Gly Asn Pro Ile Val Leu Gly Lys His Pro Asn Ser Phe Ile Cys
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 Leu Lys Arg Leu Pro Ile Gly Ser Tyr Phe
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tct ggg tgg tcc agc aca tac cgg gac ctc cgg aag ggt gtg tat gtg 99
Ser Gly Trp Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val Tyr Val
      1                      5                      10

ccc tac acc cag ggc aag tgg gaa ggg gag ctg ggc acc gac ctg gta 147
Pro Tyr Thr Gln Gly Lys Trp Glu Gly Leu Gly Thr Asp Leu Val
      15                      20                      25                      30

agc atc ccc cat ggc ccc aac gtc act gtg cgt gcc aac att gct gcc 195
Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile Ala Ala
      35                      40                      45

atc act gaa tca gac aag ttc ttc atc aac ggc tcc aac tgg gaa ggc 243
Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp Glu Gly
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atc ctg ggg ctg gcc tat gct gag att gcc agg cct gac gac tcc ccg 291
Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp Ser Pro
      65                      70                      75

gag cct ttc ttt gac tct ctg gta aag cag acc cac gtt ccc aac ctc 339
Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro Asn Leu
      80                      85                      90

ttc tcc ctg cag ctt tgt ggt gct ggc ttc ccc ctc aac cag tct gaa 387
Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln Ser Glu
      95                      100                      105                      110

gtg ctg gcc tct gtc gga ggg agc atg atc att gga ggt atc gac cac 435
Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile Asp His
      115                      120                      125

tcg ctg tac aca ggc agt ctc tgg tat aca ccc atc cgg cgg gag tgg 483
Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg Glu Trp
      130                      135                      140

tat tat gag gtg atc att gtg cgg gtg gag atc aat gga cag gat ctg 531
Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln Asp Leu
      145                      150                      155

aaa atg gac tgc aag gag tac aac tat gac aag agc att gtg gac agt 579
Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val Asp Ser
      160                      165                      170

ggc acc acc aac ctt cgt ttg ccc aag aaa gtg ttt gaa gct gca gtc 627
Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala Ala Val
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aaa tcc atc aag gca gcc tcc tcc acg gag aag ttc cct gac ggt ttc 675
Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp Gly Phe
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tgg cta gga gag cag ctg gtg tgc tgg caa gca ggc acc acc cct tgg 723
Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr Pro Trp
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aac att ttc cca gtc atc tca ctc tac cta atg ggt gag gtt acc aac 771
Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val Thr Asn
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cag tcc ttc cgc atc acc atc ctt ccg cag caa tac ctg cgg cca gtg 819
Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg Pro Val
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gaa gat gtg gcc acg tcc caa gac gac tgt tac aag ttt gcc atc tca 867
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Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala Ile Ser
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 cag tca tcc acg ggc act gtt atg gga gct gtt atc atg gag ggc ttc 915
 Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu Gly Phe
 275 280 285
 tac gtt gtc ttt gat cgg gcc cga aaa cga att ggc ttt gct gtc agc 963
 Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala Val Ser
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 gct tgc cat gtg cac gat gag ttc agg acg gca gcg gtg gaa ggc cct 1011
 Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu Gly Pro
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 ttt gtc acc ttg gac atg gaa gac tgt ggc tac aac att cca cag aca 1059
 Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro Gln Thr
 320 325 330
 gat gag tca acc ctc atg acc ata gcc tat gtc atg gct gcc atc tgc 1107
 Asp Glu Ser Thr Leu Met Thr Ile Ala Tyr Val Met Ala Ala Ile Cys
 335 340 345 350
 gcc ctc ttc atg ctg cca ctc tgc ctc atg gtg tgt cag tgg cgc tgc 1155
 Ala Leu Phe Met Leu Pro Leu Cys Leu Met Val Cys Gln Trp Arg Cys
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 ctc cgc tgc ctg cgc cag cag cat gat gac ttt gct gat gac atc tcc 1203
 Leu Arg Cys Leu Arg Gln Gln His Asp Asp Phe Ala Asp Ile Ser
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 Leu Leu Lys
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 aaaaaaaaaa aaaa 1746

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 Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile Ala Ile Thr
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 Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp Glu Gly Ile Leu
 50 55 60
 Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp Ser Pro Glu Pro
 65 70 75
 Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro Asn Leu Phe Ser
 80 85 90 95
 Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln Ser Glu Val Leu
 100 105 110
 Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile Asp His Ser Leu

115					120					125				
Tyr	Thr	Gly	Ser	Leu	Trp	Tyr	Thr	Pro	Ile	Arg	Arg	Glu	Trp	Tyr
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Glu	Val	Ile	Ile	Val	Arg	Val	Glu	Ile	Asn	Gly	Gln	Asp	Leu	Lys
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Asp	Cys	Lys	Glu	Tyr	Asn	Tyr	Asp	Lys	Ser	Ile	Val	Asp	Ser	Gly
160					165					170				
Thr	Asn	Leu	Arg	Leu	Pro	Lys	Lys	Val	Phe	Glu	Ala	Ala	Val	Lys
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Ile	Lys	Ala	Ala	Ser	Ser	Thr	Glu	Lys	Phe	Pro	Asp	Gly	Phe	Trp
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Gly	Glu	Gln	Leu	Val	Cys	Trp	Gln	Ala	Gly	Thr	Thr	Pro	Trp	Asn
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Phe	Pro	Val	Ile	Ser	Leu	Tyr	Leu	Met	Gly	Glu	Val	Thr	Asn	Gln
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Val	Ala	Thr	Ser	Gln	Asp	Asp	Cys	Tyr	Lys	Phe	Ala	Ile	Ser	Gln
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Ser	Thr	Gly	Thr	Val	Met	Gly	Ala	Val	Ile	Met	Glu	Gly	Phe	Tyr
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Val	Phe	Asp	Arg	Ala	Arg	Lys	Arg	Ile	Gly	Phe	Ala	Val	Ser	Ala
290					295					300				
His	Val	His	Asp	Glu	Phe	Arg	Thr	Ala	Ala	Val	Glu	Gly	Pro	Phe
305					310					315				
Thr	Leu	Asp	Met	Glu	Asp	Cys	Gly	Tyr	Asn	Ile	Pro	Gln	Thr	Asp
320					325					330				
Ser	Thr	Leu	Met	Thr	Ile	Ala	Tyr	Val	Met	Ala	Ala	Ile	Cys	Ala
340					345					350				
Phe	Met	Leu	Pro	Leu	Cys	Leu	Met	Val	Cys	Gln	Trp	Arg	Cys	Leu
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ggcacg atg ttg ggg ggc cgc ctc agg ctc tgg gtc tgt gtc ttg tgc 168
Met Leu Gly Ala Arg Leu Arg Leu Trp Val Cys Ala Leu Cys
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Ser	Val	Cys	Ser	Met	Ser	Val	Leu	Arg	Ala	Tyr	Pro	Asn	Ala	Ser	Pro	
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Leu	Leu	Gly	Ser	Ser	Trp	Gly	Gly	Leu	Ile	His	Leu	Tyr	Thr	Ala	Thr	
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gcc	agg	aac	agc	tac	cac	ctg	cag	atc	cac	aag	aat	ggc	cat	gtg	gat	312
Ala	Arg	Asn	Ser	Tyr	His	Leu	Gln	Ile	His	Lys	Asn	Gly	His	Val	Asp	
		25				30					35					
ggc	gca	ccc	cat	cag	acc	atc	tac	agt	gcc	ctg	atg	atc	aga	tca	gag	360
Gly	Ala	Pro	His	Gln	Thr	Ile	Tyr	Ser	Ala	Leu	Met	Ile	Arg	Ser	Glu	
		40				45				50						
gat	gct	ggc	ttt	gtg	gtg	att	aca	ggg	gtg	atg	agc	aga	aga	tac	ctc	408
Asp	Ala	Gly	Phe	Val	Val	Ile	Thr	Gly	Val	Met	Ser	Arg	Arg	Tyr	Leu	
			60						65					70		
tgc	atg	gat	ttc	aga	ggc	aac	att	ttt	gga	tca	cac	tat	ttc	gac	ccg	456
Cys	Met	Asp	Phe	Arg	Gly	Asn	Ile	Phe	Gly	Ser	His	Tyr	Phe	Asp	Pro	
			75						80				85			
gag	aac	tgc	agg	ttc	caa	cac	cag	acg	ctg	gaa	aac	ggg	tac	gac	gtc	504
Glu	Asn	Cys	Arg	Phe	Gln	His	Gln	Thr	Leu	Glu	Asn	Gly	Tyr	Asp	Val	
		90						95				100				
tac	cac	tct	cct	cag	tat	cac	ttc	ctg	gtc	agt	ctg	ggc	cgg	gcg	aag	552
Tyr	His	Ser	Pro	Gln	Thr	His	Phe	Leu	Val	Ser	Leu	Gly	Arg	Ala	Lys	
		105					110					115				
aga	gcc	ttc	ctg	cca	ggc	atg	aac	cca	ccc	cgg	tac	tcc	cag	ttc	ctg	600
Arg	Ala	Phe	Leu	Pro	Gly	Met	Asn	Pro	Pro	Pro	Tyr	Ser	Gln	Phe	Leu	
		120				125					130				135	
tcc	cgg	agg	aac	gag	atc	ccc	cta	att	cac	ttc	aac	acc	ccc	ata	cca	648
Ser	Arg	Arg	Asn	Glu	Ile	Pro	Leu	Ile	His	Phe	Asn	Thr	Pro	Ile	Pro	
			140						145					150		
cgg	cgg	cac	acc	cgg	agc	gcc	gag	gac	gac	tgg	gag	cgg	gac	ccc	ctg	696
Arg	Arg	His	Thr	Arg	Ser	Ala	Glu	Asp	Asp	Ser	Glu	Arg	Asp	Pro	Leu	
		155						160					165			
aac	gtg	ctg	aag	ccc	cgg	gcc	cgg	atg	acc	cgg	gcc	cgg	gcc	tcc	tgt	744
Asn	Val	Leu	Lys	Pro	Arg	Ala	Arg	Met	Thr	Pro	Ala	Pro	Ala	Ser	Cys	
		170					175						180			
tca	cag	gag	ctc	ccg	agc	gcc	gag	gac	aac	agc	ccg	atg	gcc	agt	gac	792
Ser	Gln	Glu	Leu	Pro	Ser	Ala	Glu	Asp	Asn	Ser	Pro	Met	Ala	Ser	Asp	
		185					190					195				
cca	tta	ggg	gtg	gtc	agg	ggc	ggg	cga	gtg	aac	acg	cac	gct	ggg	gga	840
Pro	Leu	Gly	Val	Val	Arg	Gly	Gly	Arg	Val	Asn	Thr	His	Ala	Gly	Gly	
		200				205				210				215		
acg	ggc	ccg	gaa	ggc	tgc	cgc	ccc	ttc	gcc	aag	ttc	atc	tagggtcgct			889
Thr	Gly	Pro	Glu	Gly	Cys	Arg	Pro	Phe	Ala	Lys	Phe	Ile				
			220						225							
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gggggtccctt	ccacaggagg	tctctgtgaga	accaaccttt	gagggcccaa	tcatgggggtt											1069
tcacgcgctt	cctcactcca	tatagaacac	ctttcccaat	aggaaccccc	aacaggtaaa											1129
ctagaaattt	ccccttcacg	aaggtagaga	gaaggggtct	ctcccaacat	attttctctt											1189
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1000

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      5              10              15
cag gtc aag atc aag cag ctt ttg cag gag aat gaa gtc cag ttc ctt 214
Gln Val Lys Ile Lys Gln Leu Leu Gln Glu Asn Glu Val Gln Phe Leu
      20              25              30
gat aaa gga gat gag aat act gtc gtt gat ctt gga agc aag agg cag 262
Asp Lys Gly Asp Glu Asn Thr Val Val Asp Leu Gly Ser Lys Arg Gln
      35              40              45
tat gca gat tgt tca gag att ttc aat gat ggg tat aag ctc agt gga 310
Tyr Ala Asp Cys Ser Glu Ile Phe Asn Asp Gly Tyr Lys Leu Ser Gly
      50              55              60
ttt tac aaa atc aaa cct ctc cag agc cca gca gaa ttt tct gtt tat 358
Phe Tyr Lys Ile Lys Pro Leu Gln Ser Pro Ala Glu Phe Ser Val Tyr
      70              75              80
tgt gac atg tcc gat gga gga gga tgg act gta att cag aga cga tct 406
Cys Asp Met Ser Asp Gly Gly Gly Trp Thr Val Ile Gln Arg Arg Ser
      85              90              95
gat ggc agt gaa aac ttt aac aga gga tgg aaa gac tat gaa aat ggc 454
Asp Gly Ser Glu Asn Phe Asn Arg Gly Trp Lys Asp Tyr Glu Asn Gly
      100              105              110
ttt gga amt ttt gtc caa aaa cat ggt gaa tat tgg ctg ggc aat aaa 502
Phe Gly Xaa Phe Val Gln Lys His Gly Glu Tyr Trp Leu Gly Asn Lys
      115              120              125
aat ctt cac ttc ttg acc act caa gaa gac tac act tta aaa atc gac 550
Asn Leu His Phe Leu Thr Thr Gln Glu Asp Tyr Thr Leu Lys Ile Asp
      130              135              140
ctt gca gat ttt gaa aaa aat agc cgt tat gca caa tat aag aat ttc 598
Leu Ala Asp Phe Glu Lys Asn Ser Arg Tyr Ala Gln Tyr Asn Phe
      150              155              160
aaa gtt gga gat gaa aag aat ttc tac gag ttg aat att ggg gaa tat 646
Lys Val Gly Asp Glu Lys Asn Phe Tyr Glu Leu Asn Ile Gly Glu Tyr
      165              170              175
tct gga aca gct gga gat tcc ctt gcg ggg aat ttt cat cct gag gtg 694
Ser Gly Thr Ala Gly Asp Ser Leu Ala Gly Asn Phe His Pro Glu Val
      180              185              190
cag tgg tgg gct agt cac caa aga atg aaa ttc agc agc tgg gac aga 742
Gln Trp Trp Ala Ser His Gln Arg Met Lys Phe Ser Thr Trp Asp Arg
      195              200              205
gat cat gac aac tat gaa ggg aac tgc gca gaa gaa gat cag tct ggc 790
Asp His Asp Asn Tyr Glu Gly Asn Cys Ala Glu Glu Asp Gln Ser Gly
      210              215              220
tgg tgg ttt aac agg tgt cac tyt gca aac ctg aat ggt gta tac tac 838
Trp Trp Phe Asn Arg Cys His Xaa Ala Asn Leu Asn Gly Val Tyr Tyr
      230              235              240
agc ggc ccc tac acg gct aaa aca gac aat ggg att gtc tgg tac acc 886
Ser Gly Pro Tyr Thr Ala Lys Thr Asp Asn Gly Ile Val Trp Tyr Thr
      245              250              255
tgg cat ggg tgg tgg tat tct ctg aaa tct gtg gtt atg aaa att agg 934
Trp His Gly Trp Trp Tyr Ser Leu Lys Ser Val Val Met Lys Ile Arg
      260              265              270
cca aat gat ttt att cca aat gta att taattgtctgc tgttgggctt 981
Pro Asn Asp Phe Ile Pro Asn Val Ile
      275              280
tcgtttctgc aattcagctt tgtttaaagt gatttgaaaa atactcattc tgaacatatc 1041
catgcgcaat catgataact gttgtgagta gtgcttttca ttcttctcac ttgcctttgt 1101
tacttaagt gctttcagta cagcagatat gcaatatcca ccaataaat gtgactgtg 1161
tcaaaaaaaaa aaaaaaaaa 1179

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<210> 28
 <211> 282
 <212> PRT
 <213> Homo sapiens

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<221> UNSURE
 <222> 116
 <223> Xaa = Asn,Thr

<220>
 <221> UNSURE
 <222> 233
 <223> Xaa = Phe,Ser

<400> 28
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 1 5 10 15
 Gln Gln Val Lys Ile Lys Gln Leu Leu Glu Asn Glu Val Gln Phe
 20 25 30
 Leu Asp Lys Gly Asp Glu Asn Thr Val Val Asp Leu Gly Ser Lys Arg
 35 40 45
 Gln Tyr Ala Asp Cys Ser Glu Ile Phe Asn Asp Gly Tyr Lys Leu Ser
 50 55 60
 Gly Phe Tyr Lys Ile Lys Pro Leu Gln Ser Pro Ala Glu Phe Ser Val
 65 70 75 80
 Tyr Cys Asp Met Ser Asp Gly Gly Gly Trp Thr Val Ile Gln Arg Arg
 85 90 95
 Ser Asp Gly Ser Glu Asn Phe Asn Arg Gly Trp Lys Asp Tyr Glu Asn
 100 105 110
 Gly Phe Gly Xaa Phe Val Gln Lys His Gly Glu Tyr Trp Leu Gly Asn
 115 120 125
 Lys Asn Leu His Phe Leu Thr Thr Gln Glu Asp Tyr Thr Leu Lys Ile
 130 135 140
 Asp Leu Ala Asp Phe Glu Lys Asn Ser Arg Tyr Ala Gln Tyr Lys Asn
 145 150 155 160
 Phe Lys Val Gly Asp Glu Lys Asn Phe Tyr Glu Leu Asn Ile Gly Glu
 165 170 175
 Tyr Ser Gly Thr Ala Gly Asp Ser Leu Ala Gly Asn Phe His Pro Glu
 180 185 190
 Val Gln Trp Trp Ala Ser His Gln Arg Met Lys Phe Ser Thr Trp Asp
 195 200 205
 Arg Asp His Asp Asn Tyr Glu Gly Asn Cys Ala Glu Glu Asp Gln Ser
 210 215 220
 Gly Trp Trp Phe Asn Arg Cys His Xaa Ala Asn Leu Asn Gly Val Tyr
 225 230 235 240
 Tyr Ser Gly Pro Tyr Thr Ala Lys Thr Asp Asn Gly Ile Val Trp Tyr
 245 250 255
 Thr Trp His Gly Trp Trp Tyr Ser Leu Lys Ser Val Val Met Lys Ile
 260 265 270
 Arg Pro Asn Asp Phe Ile Pro Asn Val Ile
 275 280

<210> 29
 <211> 1118
 <212> DNA
 <213> Homo sapiens

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 <222> 1..344
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 <221> CDS
 <222> 345..1118

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 <221> polyA_site
 <222> 1103..1118

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 ttgggaacaaa ggaatagttct gctcggatcc cctgcagatc ttggggcccg agggccagtc 180
 aaccccttgga gcaggaagaa acgcaaaagt gtcaagaacc aagtcgagct gctcagagc 240
 cggcccgag tagctgcaga ctccgccgc gacgtgtgcg cgcttctctg gccagagcg 300
 agcctgtttt gtgctcgggt taagagattt gtcccagcta tacc atg ggc cgc act 356
 Met Gly Arg Thr
 cgg gaa gct ggc tgc gtg gcc gct ggt gtg gtt atc ggg gct ggt gcc 404
 Arg Glu Ala Gly Cys Val Ala Ala Gly Val Val Ile Gly Ala Gly Ala
 -15 -10 -5 1
 tgc tac tgt gta tac aga ctg gct tgg gga aga gac gag aac gag aaa 452
 Cys Tyr Cys Val Tyr Arg Leu Ala Trp Gly Arg Asp Glu Asn Glu Lys
 5 10 15
 atc tgg gac gaa gac gag gag tct acg gac acc tca kag att ggg gtt 500
 Ile Trp Asp Glu Asp Glu Glu Ser Thr Asp Thr Ser Xaa Ile Gly Val
 20 25 30
 gag act gtg aaa gga gct aaa act aac gct ggg gca ggg tct ggg gcc 548
 Glu Thr Val Lys Gly Ala Lys Thr Asn Ala Gly Ala Gly Ser Gly Ala
 35 40 45
 aaa ctt cag ggt gat tca gag gtc aag cct gag gtg agt ttg gga ctg 596
 Lys Leu Gln Gly Asp Ser Glu Val Lys Pro Glu Val Ser Leu Gly Leu
 50 55 60 65
 gag gat tgt ccg ggt gta aaa gag aag gcc cat tca gga tcc cac agc 644
 Glu Asp Cys Pro Gly Val Lys Glu Lys Ala His Ser Gly Ser His Ser
 70 75 80
 gga ggt ggc cta gag gcc aag gcc aag gcc ctt ttc aac acg ctg aag 692
 Gly Gly Glu Leu Glu Ala Lys Ala Lys Ala Leu Phe Asn Thr Leu Lys
 85 90 95
 gaa cag gca agt gca aag gca gcc aaa ggg gct agg gtg ggt acc atc 740
 Glu Gln Ala Ser Ala Lys Ala Gly Lys Gly Ala Arg Val Gly Thr Ile
 100 105 110
 tct ggg aac agg acc ctt gca ccg agt tta ccc tgc cca gga ggc agg 788
 Ser Gly Asn Arg Thr Leu Ala Pro Ser Leu Pro Cys Pro Gly Gly Arg
 115 120 125
 ggt gga ggc tgc cac ccc acc agg agt gga tct agg gcc ggg ggc agg 836
 Gly Gly Gly Cys His Pro Thr Arg Ser Gly Ser Arg Ala Gly Gly Arg
 130 135 140 145
 gca agt gga aaa tcc aag gga aag gcc cga agt aag agc acc agg gct 884
 Ala Ser Gly Lys Ser Lys Gly Lys Ala Arg Ser Lys Ser Thr Arg Ala
 150 155 160
 cca gct aca aca tgg cct gtc cgg aga ggc aag ttc aac ttt cct tat 932
 Pro Ala Thr Thr Trp Pro Val Arg Arg Gly Lys Phe Asn Phe Pro Tyr
 165 170 175
 aaa att gat gat att ctg agt gct ccc gac ctc caa aag gtc ctc aac 980
 Lys Ile Asp Asp Ile Leu Ser Ala Pro Asp Leu Gln Lys Val Leu Asn
 180 185 190
 atc ctg gag cga aca aat gat cct ttt att caa gaa gta gcc ttg gtc 1028
 Ile Leu Glu Arg Thr Asn Asp Pro Phe Ile Gln Glu Val Ala Leu Val
 195 200 205
 act ctg ggt aac aat gca gca tat tca ttt aac cag aat gcc ata cgt 1076
 Thr Leu Gly Asn Asn Ala Ala Tyr Ser Phe Asn Gln Asn Ala Ile Arg
 210 215 220 225
 gaa ttg ggt ggt gtc cca att att gca aaa aaa aaa aaa 1118
 Glu Leu Gly Gly Val Pro Ile Ile Ala Lys Lys Lys Lys Lys
 230 235
 <210> 30
 <211> 258
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..20

<220>
 <221> UNSURE
 <222> 49
 <223> Xaa = Glu, *

<400> 30
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 -20 -15 -10 -5
 Gly Ala Gly Ala Cys Tyr Cys Val Tyr Arg Leu Ala Trp Gly Arg Asp
 1 5 10
 Glu Asn Glu Lys Ile Trp Asp Glu Asp Glu Glu Ser Thr Asp Thr Ser
 15 20 25
 Xaa Ile Gly Val Glu Thr Val Lys Gly Ala Lys Thr Asn Ala Gly Ala
 30 35 40
 Gly Ser Gly Ala Lys Leu Gln Gly Asp Ser Glu Val Lys Pro Glu Val
 45 50 55 60
 Ser Leu Gly Leu Glu Asp Cys Pro Gly Val Lys Glu Lys Ala His Ser
 65 70 75
 Gly Ser His Ser Gly Gly Gly Leu Ala Lys Ala Lys Ala Leu Phe
 80 85 90
 Asn Thr Leu Lys Glu Gln Ala Ser Ala Lys Ala Gly Lys Gly Ala Arg
 95 100 105
 Val Gly Thr Ile Ser Gly Asn Arg Thr Leu Ala Pro Ser Leu Pro Cys
 110 115 120
 Pro Gly Gly Arg Gly Gly Cys His Pro Thr Arg Ser Gly Ser Arg
 125 130 135 140
 Ala Gly Gly Arg Ala Ser Gly Lys Ser Lys Gly Lys Ala Arg Ser Lys
 145 150 155
 Ser Thr Arg Ala Pro Ala Thr Thr Trp Pro Val Arg Arg Gly Lys Phe
 160 165 170
 Asn Phe Pro Tyr Lys Ile Asp Asp Ile Leu Ser Ala Pro Asp Leu Gln
 175 180 185
 Lys Val Leu Asn Ile Leu Glu Arg Thr Asn Asp Pro Phe Ile Gln Glu
 190 195 200
 Val Ala Leu Val Thr Leu Gly Asn Asn Ala Ala Tyr Ser Phe Asn Gln
 205 210 215 220
 Asn Ala Ile Arg Glu Leu Gly Gly Val Pro Ile Ile Ala Lys Lys Lys
 225 230 235
 Lys Lys

<210> 31
 <211> 1273
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 1..13

<220>
 <221> CDS
 <222> 14..1048

<220>
 <221> 3'UTR
 <222> 1049..1273

<220>
 <221> polyA_signal

[illegible]

<221> polyA site

<400> 31

28

260 cat ctt ggg gga gct ctt ttt gga ata tgg tat gtt act tac ggt cat 961
 His Leu Gly Gly Ala Leu Phe Gly Ile Trp Tyr Val Thr Tyr Gly His
 280 285 290
 gaa ctg att tgg aag aac agg gag cgg cta gtg aaa atc tgg cat gaa 1009
 Glu Leu Ile Trp Lys Asn Arg Glu Pro Leu Val Lys Ile Trp His Glu
 295 300 305
 ata agg act aat ggc ccc aaa aaa gga ggt ggc tct aag taaaactggg 1058
 Ile Arg Thr Asn Gly Pro Lys Lys Gly Gly Ser Lys
 310 315 320
 attggacagt agtgggtgcat ctggtctcttg ccgcctgaga gccccaggag acatcggtcta 1118
 gagtgaccat ggctatgctc ccgtctgtgaa gatgccagca tctggcctcc cacttttttc 1178
 agctgtgtcc ccagtcctgt gtcttttttag aatgtgaatg atgataaagt tgtgaaataa 1238
 aggtttctat ctagtttgca aaaaaaaaaa aaaaa 1273

<210> 32
 <211> 345
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..26

<400> 32
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 -25 -20 -15
 Trp Gly Ala Ser Val Gly Gly Arg Ser Cys Glu Leu Thr Ala Val
 -10 -5 1 5
 Leu Thr Pro Pro Gln Leu Leu Gly Arg Arg Phe Asn Phe Phe Ile Gln
 10 15 20
 Gln Lys Cys Gly Phe Arg Lys Ala Pro Arg Lys Val Glu Pro Arg Arg
 25 30 35
 Ser Asp Pro Gly Thr Ser Gly Glu Ala Tyr Lys Arg Ser Ala Leu Ile
 40 45 50
 Pro Pro Val Glu Glu Thr Val Phe Tyr Pro Ser Pro Tyr Pro Ile Arg
 55 60 65 70
 Ser Leu Ile Lys Pro Leu Phe Phe Thr Val Gly Phe Thr Gly Cys Ala
 75 80 85
 Phe Gly Ser Ala Ala Ile Trp Gln Tyr Glu Ser Leu Lys Ser Arg Val
 90 95 100
 Gln Ser Tyr Phe Asp Gly Ile Lys Ala Asp Trp Leu Asp Ser Ile Arg
 105 110 115
 Pro Gln Lys Glu Gly Asp Phe Arg Lys Glu Ile Asn Lys Trp Trp Asn
 120 125 130
 Asn Leu Ser Asp Gly Gln Arg Thr Val Thr Gly Ile Ile Ala Ala Asn
 135 140 145 150
 Val Leu Val Phe Cys Leu Trp Arg Val Pro Ser Leu Gln Arg Thr Met
 155 160 165
 Ile Arg Tyr Phe Thr Ser Asn Pro Ala Ser Lys Val Leu Cys Ser Pro
 170 175 180
 Met Leu Leu Ser Thr Phe Ser His Phe Ser Leu Phe His Met Ala Ala
 185 190 195
 Asn Met Tyr Val Leu Trp Ser Phe Ser Ser Ser Ile Val Asn Ile Leu
 200 205 210
 Gly Gln Glu Gln Phe Met Ala Val Tyr Leu Ser Ala Gly Val Ile Ser
 215 220 225 230
 Asn Phe Val Ser Tyr Val Gly Lys Val Ala Thr Gly Arg Tyr Gly Pro
 235 240 245
 Ser Leu Gly Ala Ala Leu Lys Ala Ile Ile Ala Met Asp Thr Ala Gly
 250 255 260
 Met Ile Leu Gly Trp Lys Phe Phe Asp His Ala Ala His Leu Gly Gly
 265 270 275

Ala Leu Phe Gly Ile Trp Tyr Val Thr Tyr Gly His Glu Leu Ile Trp
 280 285 290
 Lys Asn Arg Glu Pro Leu Val Lys Ile Trp His Glu Ile Arg Thr Asn
 295 300 305 310
 Gly Pro Lys Lys Gly Gly Ser Lys
 315

<210> 33
 <211> 723
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..72

<220>
 <221> CDS
 <222> 73..672

<220>
 <221> 3'UTR
 <222> 673..723

<220>
 <221> polyA_signal
 <222> 689..694

<220>
 <221> polyA_site
 <222> 708..723

<400> 33
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 accgacacca tc atg gat tca agc acc gca cac agt ccg gtg ttt ctg gta 111
 Met Asp Ser Ser Thr Ala His Ser Pro Val Phe Leu Val
 1 5 10
 ttt cct cca gaa atc act gct tca gaa tat gag tcc aca gaa ctt tca 159
 Phe Pro Pro Glu Ile Thr Ala Ser Glu Tyr Glu Ser Thr Glu Leu Ser
 15 20 25
 gcc acg acc ttt tca act caa agc ccc ttg caa aaa tta ttt gct aga 207
 Ala Thr Thr Phe Ser Thr Gln Ser Pro Leu Gln Lys Leu Phe Ala Arg
 30 35 40 45
 aaa atg aaa atc tta ggg act atc cag atc ctg ttt gga att atg acc 255
 Lys Met Lys Ile Leu Gly Thr Ile Gln Ile Leu Phe Gly Ile Met Thr
 50 55 60
 ttt tct ttt gga gtt atc ttc ctt ttc acc ttg tta aaa cca tat cca 303
 Phe Ser Phe Gly Val Ile Phe Leu Phe Thr Leu Leu Lys Pro Tyr Pro
 65 70 75
 agg ttt ccc ttt ata ttt ctt tca gga tat cca ttc tgg ggc tct gtt 351
 Arg Phe Pro Phe Ile Phe Leu Ser Gly Tyr Pro Phe Trp Gly Ser Val
 80 85 90
 ttg ttc att aat tct gga gcc ttc cta att gca gtg aaa aga aaa acc 399
 Leu Phe Ile Asn Ser Gly Ala Phe Leu Ile Ala Val Lys Arg Lys Thr
 95 100 105
 aca gaa act ctg ata ata ttg agc cga ata atg aat ttt ctt agt gcc 447
 Thr Glu Thr Leu Ile Ile Leu Ser Arg Ile Met Asn Phe Leu Ser Ala
 110 115 120 125
 ctg gga gca ata gct gga atc att ctc ctc aca ttt ggt ttc atc cta 495
 Leu Gly Ala Ile Ala Gly Ile Ile Leu Leu Thr Phe Gly Phe Ile Leu
 130 135 140
 gat caa aac tac att tgt ggt tat tct cac caa aat agt cag tgt aag 543
 Asp Gln Asn Tyr Ile Cys Gly Tyr Ser His Gln Asn Ser Gln Cys Lys

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          145          150          155          591
gct gtt act gtc ctg ttc ttg gga att ttg att aca ttg atg act ttc
Ala Val Thr Val Leu Phe Leu Gly Ile Leu Ile Thr Leu Met Thr Phe
          160          165          170
agc att att gaa tta ttc att tct ctg cct ttc tca att ttg ggg tgc 639
Ser Ile Ile Glu Leu Phe Ile Ser Leu Pro Phe Ser Ile Leu Gly Cys
          175          180          185
cac tca gag gat tgt gat tgt gaa caa tgt tgt tgactagcac tgtgagaata 692
His Ser Glu Asp Cys Asp Cys Glu Gln Cys Cys
          190          195          200
aagatgtgtt aaaataaaaa aaaaaaaaaa t
          723

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<210> 34
<211> 200
<212> PRT
<213> Homo sapiens

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<400> 34
Met Asp Ser Ser Thr Ala His Ser Pro Val Phe Leu Val Phe Pro Pro
1          5          10          15
Glu Ile Thr Ala Ser Glu Tyr Glu Ser Thr Glu Leu Ser Ala Thr Thr
          20          25          30
Phe Ser Thr Gln Ser Pro Leu Gln Lys Leu Phe Ala Arg Lys Met Lys
          35          40          45
Ile Leu Gly Thr Ile Gln Ile Leu Phe Gly Ile Met Thr Phe Ser Phe
          50          55          60
Gly Val Ile Phe Leu Phe Thr Leu Leu Lys Pro Tyr Pro Arg Phe Pro
          65          70          75          80
Phe Ile Phe Leu Ser Gly Tyr Pro Phe Trp Gly Ser Val Leu Phe Ile
          85          90          95
Asn Ser Gly Ala Phe Leu Ile Ala Val Lys Arg Lys Thr Thr Glu Thr
          100          105          110
Leu Ile Ile Leu Ser Arg Ile Met Asn Phe Leu Ser Ala Leu Gly Ala
          115          120          125
Ile Ala Gly Ile Ile Leu Leu Thr Phe Gly Phe Ile Leu Asp Gln Asn
          130          135          140
Tyr Ile Cys Gly Tyr Ser His Gln Asn Ser Gln Cys Lys Ala Val Thr
          145          150          155          160
Val Leu Phe Leu Gly Ile Leu Ile Thr Leu Met Thr Phe Ser Ile Ile
          165          170          175
Glu Leu Phe Ile Ser Leu Pro Phe Ser Ile Leu Gly Cys His Ser Glu
          180          185          190
Asp Cys Asp Cys Glu Gln Cys Cys
          195          200

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<210> 35
<211> 845
<212> DNA
<213> Homo sapiens

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<220>
<221> 5'UTR
<222> 1..118

<220>
<221> CDS
<222> 119..655

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<220>
<221> 3'UTR
<222> 656..845

<220>

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<221> polyA_signal

<222> 809..814

<220>

<221> polyA_site

<222> 830..845

<400> 35

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taaattctgc caaaaggact gaggaacggg gcctggaaaaa gggcaagaat atcacggc 118
atg ggc atg agt agc ttg aaa ctg ctg aag tat gtc ctg ttt ttc ttc 166
Met Gly Met Ser Ser Leu Lys Leu Leu Lys Tyr Val Leu Phe Phe Phe
1 5 10 15
aac ttg ctc ttt tgg atc tgt ggc tgc tgc att ttg ggc ttt ggg atc 214
Asn Leu Leu Phe Trp Ile Cys Gly Cys Cys Ile Leu Gly Phe Gly Ile
20 25 30
tac ctg ctg atc cac aac aac ttc gga gtg ctc ttc cat aac ctc ccc 262
Tyr Leu Leu Ile His Asn Asn Phe Gly Val Leu Phe His Asn Leu Pro
35 40 45
ttc ctc acg ctg ggc aat gtg ttt gtc atc gtg ggc tct att atc atg 310
Ser Leu Thr Leu Gly Asn Val Phe Val Ile Val Gly Ser Ile Ile Met
50 55 60
gta gtt gcc ttc ctg ggc tgc atg ggc tct atc aag gaa aac aag tgt 358
Val Val Ala Phe Leu Gly Cys Met Gly Ser Ile Lys Glu Asn Lys Cys
65 70 75 80
ctg ctt atg tgc ttc ttc atc ctg ctg ctg att atc ctc ctt gct gag 406
Leu Leu Met Ser Phe Phe Ile Leu Leu Leu Ile Ile Leu Ala Glu
85 90 95
gtg acc ttg gcc atc ctg ctc ttt gtg gct aag ggt ctg acc gac agc 454
Val Thr Leu Ala Ile Leu Leu Phe Val Ala Lys Gly Leu Thr Asp Ser
100 105 110
atc cac cgt tac cac tca gac aat agc acc aag gca gcg tgg gac tcc 502
Ile His Arg Tyr His Ser Asp Asn Ser Thr Lys Ala Ala Trp Asp Ser
115 120 125
atc cag tca ttt ctg cag tgt tgt ggt ata aat ggc acg agt gat tgg 550
Ile Gln Ser Phe Leu Gln Cys Cys Gly Ile Asn Gly Thr Ser Asp Trp
130 135 140
acc agt ggc cca cca gca tct tgc ccc tca gat cga aaa gtg gag ggt 598
Thr Ser Gly Pro Pro Ala Ser Cys Pro Ser Asp Arg Lys Val Glu Gly
145 150 155 160
tgc tat gcg aaa gca aga ctg tgg ttt cat tcc aat ttc ttt att aga 646
Cys Tyr Ala Lys Ala Arg Leu Trp Phe His Ser Asn Phe Phe Ile Arg
165 170 175
ggg cct tat tgatgtgttc taagtctttc cagaaaaaaa ctatccagtg 695
Gly Pro Tyr
atttatatcc tgatttcaac cagtcactta gctgataatc acagtaagaa gacttctggt 755
attatctctc tatcagataaa gattttgtta atgtactatt ttactcttca ataaataaaa 815
cagtttatta tcgcaaaaaa aaaaaaaaaa 845
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<210> 36

<211> 179

<212> PRT

<213> Homo sapiens

<400> 36

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Met Gly Met Ser Ser Leu Lys Leu Leu Lys Tyr Val Leu Phe Phe Phe
1 5 10 15
Asn Leu Leu Phe Trp Ile Cys Gly Cys Cys Ile Leu Gly Phe Gly Ile
20 25 30
Tyr Leu Leu Ile His Asn Asn Phe Gly Val Leu Phe His Asn Leu Pro
35 40 45
Ser Leu Thr Leu Gly Asn Val Phe Val Ile Val Gly Ser Ile Ile Met
50 55 60
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Val Val Ala Phe Leu Gly Cys Met Gly Ser Ile Lys Glu Asn Lys Cys
65 70 75 80
Leu Leu Met Ser Phe Phe Ile Leu Leu Leu Ile Ile Leu Leu Ala Glu
85 90 95
Val Thr Leu Ala Ile Leu Leu Phe Val Ala Lys Gly Leu Thr Asp Ser
100 105 110
Ile His Arg Tyr His Ser Asp Asn Ser Thr Lys Ala Ala Trp Asp Ser
115 120 125
Ile Gln Ser Phe Leu Gln Cys Cys Gly Ile Asn Gly Thr Ser Asp Trp
130 135 140
Thr Ser Gly Pro Pro Ala Ser Cys Pro Ser Asp Arg Lys Val Glu Gly
145 150 155 160
Cys Tyr Ala Lys Ala Arg Leu Trp Phe His Ser Asn Phe Phe Ile Arg
165 170 175
Gly Pro Tyr

<210> 37

<211> 517

<212> DNA

<213> Homo sapiens

<220>

<221> 5'UTR

<222> 1..16

<220>

<221> CDS

<222> 17..259

<220>

<221> 3'UTR

<222> 260..517

<400> 37

ttccatagaa tgggag atg tca cca ggg cag cct atg aca ttc ccc cca gag 52
Met Ser Pro Gly Gln Pro Met Thr Phe Pro Pro Glu
1 5 10

gcc ctg tgg gtg acc gtg ggg ctg tct gtc tgt ctc att gca ctg ctg 100
Ala Leu Trp Val Thr Val Gly Leu Ser Val Cys Leu Ile Ala Leu Leu
15 20 25

gtg gcc ctg gct ttc gtg tgc tgg aga aag atc aaa cag agc tgt gag 148
Val Ala Leu Ala Phe Val Cys Trp Arg Lys Ile Lys Gln Ser Cys Glu
30 35 40

gag gag aat gca gga gct gag gac cag gat ggg gag gga gaa ggc tcc 196
Glu Glu Asn Ala Gly Ala Glu Asp Gln Asp Gly Glu Gly Glu Gly Ser
45 50 55

aag aca gcc ctg cag cct ctg aaa cac tct gac agc aaa gaa gat gat 244
Lys Thr Ala Leu Gln Pro Leu Lys His Ser Asp Ser Lys Glu Asp Asp
65 70 75

gga caa gaa ata gcc tgaccatgag gaccaggag ctgctacccc tccctacagc 299
Gly Gln Glu Ile Ala
80

tcctaccctc tggctgcaat ggggctgcac tgtgagccct gccccaaca gatgcacct 359
gctctgacag gtgggctcct tctccaaagg atgcgataca cagaccactg tgcagcctta 419
tttctccaat ggacatgatt cccaagtcat cctgctgcct tttttcttat agacacaatg 479
aacagaccac ccacaacctt agttctctaa gtcatect 517

<210> 38

<211> 81

<212> PRT

<213> Homo sapiens

<400> 38

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 Thr Val Gly Leu Ser Val Cys Leu Ile Ala Leu Leu Val Ala Leu Ala
 20 25 30
 Phe Val Cys Trp Arg Lys Ile Lys Gln Ser Cys Glu Glu Glu Asn Ala
 35 40 45
 Gly Ala Glu Asp Gln Asp Gly Glu Gly Glu Gly Ser Lys Thr Ala Leu
 50 55 60
 Gln Pro Leu Lys His Ser Asp Ser Lys Glu Asp Asp Gly Gln Glu Ile
 65 70 75 80
 Ala

<210> 39
 <211> 1816
 <212> DNA
 <213> Homo sapiens

<220>
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<220>
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 <222> 260..1048

<220>
 <221> 3'UTR
 <222> 1049..1816

<220>
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 <222> 1782..1787

<220>
 <221> polyA_site
 <222> 1801..1816

<400> 39
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 gcctcaacttc gtcccaactgt ggtaggggtt gaggctctgc aatgttaagt gatttgctca 180
 aggtgcccat ttgcaggaa ttggagccca gccagttct ctgagcctat cattagggct 240
 aaaggagtgc gtgatcaga atg gtg tct gga cgg ttc tac ttg tcc tgc ctg 292
 Met Val Ser Gly Arg Phe Tyr Leu Ser Cys Leu
 -15 -10
 ctg ctg ggg tcc ctg ggc tct atg tgc atc etc ttc act atc tac tgg 340
 Leu Leu Gly Ser Leu Gly Ser Met Cys Ile Leu Phe Thr Ile Tyr Trp
 -5 1 5
 atg cag tac tgg cgt ggt ggc ttt gcc tgg aat ggc agc atc tac atg 388
 Met Gln Tyr Trp Arg Gly Gly Phe Ala Trp Asn Gly Ser Ile Tyr Met
 10 15 20
 ttc aac tgg cac cca gtg ctt atg gtt gct ggc atg gtg gta ttc tat 436
 Phe Asn Trp His Pro Val Leu Met Val Ala Gly Met Val Val Phe Tyr
 25 30 35 40
 gga ggt gcg tca ctg gtg tac cgc ctg ccc cag tgg gtg ggg ccc 484
 Gly Gly Ala Ser Leu Val Tyr Arg Leu Pro Gln Ser Trp Val Gly Pro
 45 50 55
 aaa ctg ccc tgg aaa atc etc cat gca gcg ctg cac ctg atg gcc ttc 532
 Lys Leu Pro Trp Lys Leu Leu His Ala Ala Leu His Leu Met Ala Phe
 60 65 70
 gtc etc act gtt gtg ggg ctg gtt gct gtc ttt acg ttt cac aac cat 580
 Val Leu Thr Val Val Gly Leu Val Ala Val Phe Thr Phe His Asn His
 75 80 85

gga agg act gcc aac ctc tac tcc ctt cac agc tgg ctg ggc atc acc 628
 Gly Arg Thr Ala Asn Leu Tyr Ser Leu His Ser Trp Leu Gly Ile Thr
 90 95 100
 act gtc ttc ctc ttc ggc tgc cag tgg ttc ctg ggc ttt gct gtc ttc 676
 Thr Val Phe Leu Phe Gly Cys Gln Trp Phe Leu Gly Phe Ala Val Phe
 105 110 115 120
 ctc ctg ccc tgg gcg tcc atg tgg ctg cgc agc ctc cta aaa cct atc 724
 Leu Leu Pro Trp Ala Ser Met Trp Leu Arg Ser Leu Leu Lys Pro Ile
 125 130 135
 cac gtc ttt ttt gga gcc gcc atc ctc tct ctg tcc atc gca tcc gtc 772
 His Val Phe Phe Gly Ala Ala Ile Leu Ser Leu Ser Ile Ala Ser Val
 140 145 150
 att tcg ggc att aat gag aag ctt ttc ttc agt ttg aaa aac acc acc 820
 Ile Ser Gly Ile Asn Glu Lys Leu Phe Phe Ser Leu Lys Asn Thr Thr
 155 160 165
 agg cca tac cac agc ctg ccc agt gag gcg gtc ttt gcc aac agc acc 868
 Arg Pro Tyr His Ser Leu Pro Ser Glu Ala Val Phe Ala Asn Ser Thr
 170 175 180
 ggg atg ctg gtg gtg gcc ttt ggg ctg ctg gtg ctc tac atc ctt ctg 916
 Gly Met Leu Val Val Ala Phe Gly Leu Leu Val Leu Tyr Ile Leu Leu
 185 190 195 200
 gct tca tct tgg aag cgc cca gag ccg ggg atc ctg acc gac aga cag 964
 Ala Ser Ser Trp Lys Arg Pro Glu Pro Gly Ile Leu Thr Asp Arg Gln
 205 210 215
 ctg ctg cta cag ctg agg cct gga tcc cgg cct ttc cct gtg act tac 1012
 Leu Leu Leu Gln Leu Arg Pro Gly Ser Arg Pro Phe Pro Val Thr Tyr
 220 225 230
 gtg tct gtc acc ggc agg cag ccc tac aaa tcc tgg tgacctgtctc 1058
 Val Ser Val Thr Gly Arg Gln Pro Tyr Lys Ser Trp
 235 240
 tcccaagaac agagcctgtc cccagatgtc ccagtagcga tgaagtaacag aggtggctgt 1118
 ggacttctct taacttctct tgctggatca gggccttctc gctcccgctc gggcaggtct 1178
 ggccttctct tcttgccagg gccccagccc ctctgaccac ctctgagctc accatgcagc 1238
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 gaccgtcttg actggctgga gccttcaaag ccactgggat gtcctccagg cactggggtc 1718
 ccactgaccag ctcccgctct ccataggggg aggcatttca ctggttttatg aagctcgagt 1778
 ttcattaaat atgttaagaa tcaaaaaaaa aaaaaaaa 1816

<210> 40
 <211> 263
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..20

<400> 40
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 -20 -15 -10 -5
 Gly Ser Met Cys Ile Leu Phe Thr Ile Tyr Trp Met Gln Tyr Trp Arg
 1 5 10
 Gly Gly Phe Ala Trp Asn Gly Ser Ile Tyr Met Phe Asn Trp His Pro
 15 20 25
 Val Leu Met Val Ala Gly Met Val Val Phe Tyr Gly Gly Ala Ser Leu
 30 35 40
 Val Tyr Arg Leu Pro Gln Ser Trp Val Gly Pro Lys Leu Pro Trp Lys

Ala Asp Gln Asn Cys Thr Gln Glu Cys Val Ser Asp Ser Glu Cys Ala
15 20 25
gac aac ctc aag tgc tgc agc gcg ggc tgt gcc acc ttc tgc tct ctg 306
Asp Asn Leu Lys Cys Cys Ser Ala Gly Cys Ala Thr Phe Cys Ser Leu
30 35 40
ccc aat gat aag gag ggt tcc tgc ccc cag gtg aac att aac ttt ccc 354
Pro Asn Asp Lys Glu Gly Ser Cys Pro Gln Val Asn Ile Asn Phe Pro
45 50 55
cag ctc ggc ctc tgt cgg gac cag tgc cag gtg gac agc cag tgt cct 402
Gln Leu Gly Leu Cys Arg Asp Gln Cys Gln Val Asp Ser Gln Cys Pro
60 65 70 75
ggc cag atg aaa tgc tgc cgc aat ggc tgt ggg aag gtg tcc tgt gtc 450
Gly Gln Met Lys Cys Cys Arg Asn Gly Cys Gly Lys Val Ser Cys Val
80 85 90
act ccc aat ttc tgagctccag ccaccaccag gctgagcagt gaggagagaa 502
Thr Pro Asn Phe
95
agttttctgcc tggccctgca tctggttcca gccacactgc cctccccctt ttcgggactc 562
tgtattccct cttgggctga ccacagcttc tccctttccc aaccaataaa gtaaccactt 622
tcagcaaaaa aaaaaaaaaa a 643

<210> 42
<211> 124
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> 1..30

<400> 42
Met Pro Ala Cys Arg Leu Gly Pro Leu Ala Ala Leu Leu Leu Ser
-30 -25 -20 -15
Leu Leu Leu Phe Gly Phe Thr Leu Val Ser Gly Thr Gly Ala Glu Lys
-10 -5 1
Thr Gly Val Cys Pro Glu Leu Gln Ala Asp Gln Asn Cys Thr Gln Glu
5 10 15
Cys Val Ser Asp Ser Glu Cys Ala Asp Asn Leu Lys Cys Cys Ser Ala
20 25 30
Gly Cys Ala Thr Phe Cys Ser Leu Pro Asn Asp Lys Glu Gly Ser Cys
35 40 45 50
Pro Gln Val Asn Ile Asn Phe Pro Gln Leu Gly Leu Cys Arg Asp Gln
55 60 65
Cys Gln Val Asp Ser Gln Cys Pro Gly Gln Met Lys Cys Cys Arg Asn
70 75 80
Gly Cys Gly Lys Val Ser Cys Val Thr Pro Asn Phe
85 90

<210> 43
<211> 501
<212> DNA
<213> Homo sapiens

<220>
<221> 5'UTR
<222> 1..227

<220>
<221> CDS
<222> 228..501

<400> 43
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ctgatctcaa atcgagctgt gactaaaacc tctaggtgct gtgctgtcct gaggcctggg 180
ccatggtgcc caaggaaagc ccctgaagct caccaggagg aagaagc atg cag ggc 236
Met Gln Gly
-30
act cct gga ggc ggg acg cgc cct ggg cca tcc ccc gtg gac agg cgg 284
Thr Pro Gly Gly Gly Thr Arg Pro Gly Pro Ser Pro Val Asp Arg Arg
-25 -20 -15
aca ctc ctg gtc ttc agc ttt atc ctg gca gca gct ttg ggc caa atg 332
Thr Leu Leu Val Phe Ser Phe Ile Leu Ala Ala Ala Leu Gly Gln Met
-10 -5 1
aat ttc aca ggg gac cag gtt ctt cga gtc ctg gcc aaa gat gag aag 380
Asn Phe Thr Gly Asp Gln Val Leu Arg Val Leu Ala Lys Asp Gly Lys
5 10 15
cag ctt tca ctt ctc ggg gat ctg gag ggc ctg aaa ccc cag aag gtg 428
Gln Leu Ser Leu Leu Gly Asp Leu Glu Gly Leu Lys Pro Gln Lys Val
20 25 30 35
gac ttc tgg cgt ggc cca gcc agg ccc agc ctc cct gtg gat atg aga 476
Asp Phe Trp Arg Gly Pro Ala Arg Pro Ser Leu Pro Val Asp Met Arg
40 45 50
gtt cct ttc tcc gaa ctg aaa gac a 501
Val Pro Phe Ser Glu Leu Lys Asp
55

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<210> 44
<211> 91
<212> PRT
<213> Homo sapiens

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<220>
<221> SIGNAL
<222> 1..33

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<400> 44
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-30 -25 -20
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-15 -10 -5
Gly Gln Met Asn Phe Thr Gly Asp Gln Val Leu Arg Val Leu Ala Lys
1 5 10 15
Asp Glu Lys Gln Leu Ser Leu Leu Gly Asp Leu Glu Gly Leu Lys Pro
20 25 30
Gln Lys Val Asp Phe Trp Arg Gly Pro Ala Arg Pro Ser Leu Pro Val
35 40 45
Asp Met Arg Val Pro Phe Ser Glu Leu Lys Asp
50 55

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<210> 45
<211> 960
<212> DNA
<213> Homo sapiens

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<220>
<221> 5'UTR
<222> 1..97

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<220>
<221> CDS
<222> 98..934

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<220>
<221> 3'UTR
<222> 935..960

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<400> 45

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cgggcccgttt	caccccgagg	aggaaggaca	ctgggttc	atg acg cca tca gaa ggc	115	
				Met Thr Pro Ser Gln Gly		
				1	5	
gcc aga gca ggg acc gga cgc gag ttg gag atg ttg gac tcg ctg ttg	163					
Ala Arg Ala Gly Thr Gly Arg Glu Leu Glu Met Leu Asp Ser Leu Leu						
	10		15		20	
gcc ttg ggc ggc ctg gtg ctg ctt cgg gat tcc gtg gag tgg gag ggg	211					
Ala Leu Gly Gly Leu Val Leu Leu Arg Asp Ser Val Gln Trp Glu Gly						
	25		30		35	
cgc agt ctc ttg aag cgc ctt gtc aag aaa tct gca ctg tgt ggg gag	259					
Arg Ser Leu Leu Cys Ala Leu Val Lys Ser Leu Ala Leu Cys Gln Gly						
	40		45		50	
caa gtg cat atc ctg ggc tgt gaa gtg agc gag gaa gag ttt cgt gaa	307					
Gln Val His Ile Leu Gly Cys Glu Val Ser Glu Glu Glu Phe Arg Glu						
	55		60		65	
ggg ttt gac tct gat atc aac aat cgg ctg gtt tac cat gac ttc ttc	355					
Gly Phe Asp Ser Asp Ile Asn Asn Arg Leu Val Tyr His Asp Phe Phe						
	75		80		85	
aga gac cct ctc aac tgg tca aya act gag gag gcc ttt cct ggg ggg	403					
Arg Asp Pro Leu Asn Trp Ser Lys Thr Glu Glu Ala Phe Pro Gln Gly						
	90		95		100	
ccg ctg gga gcc ttg aga gcc atg tgc aag agg aca gat cct gtt cct	451					
Pro Leu Gly Ala Leu Arg Ala Met Cys Lys Arg Thr Asp Pro Val Pro						
	105		110		115	
gtc acc att gct ctc gat tca ctc agc tgg ctg cta ctt cgc ctt ccc	499					
Val Thr Ile Ala Leu Asp Ser Leu Ser Trp Leu Leu Arg Leu Pro						
	120		125		130	
tgc acc aca ctc tgc cag gtc ctg cat gct gtg agc cat cag gac tct	547					
Cys Thr Thr Leu Cys Gln Val Leu His Ala Val Ser His Gln Asp Ser						
	135		140		145	
tgt cct ggt gac agc tcc tca gtg ggg aaa gtg agt gtg ctg ggc ttg	595					
Cys Pro Gly Asp Ser Ser Ser Val Gly Lys Val Ser Val Leu Gly Leu						
	155		160		165	
cta cat gaa gag ctt cat gga cca ggc cct gtg gga gct ctc agc agc	643					
Leu His Glu Glu Leu His Gly Pro Gly Pro Val Gly Ala Leu Ser Ser						
	170		175		180	
ctt gct cag act gat gag gtg acc ctg ggc ggt acc atg ggc cag gcc tcg	691					
Leu Ala Gln Thr Glu Val Thr Leu Gly Gly Thr Met Gly Gln Ala Ser						
	185		190		195	
gcc cac atc ctg tgt cgg agg ccc cga cag cgc cca act gac cag act	739					
Ala His Ile Leu Cys Arg Arg Pro Arg Gln Arg Pro Thr Asp Gln Thr						
	200		205		210	
cag tgg ttc tcc atc ctt ccg gac ttc agc ctg gat ctc caa gag ggg	787					
Gln Trp Phe Ser Ile Leu Pro Asp Phe Ser Leu Asp Leu Gln Glu Gly						
	215		220		225	
ccc tct gta gag tcc cag ccc tcc gat cct cat ata ccc ccg gta	835					
Pro Ser Val Glu Ser Gln Pro Tyr Ser Asp Pro His Ile Pro Pro Val						
	235		240		245	
tct aag aat gcc aag gcc aga aca agg aaa tgt agt tta gta tct ggt	883					
Ser Lys Asn Ala Lys Ala Arg Thr Arg Lys Cys Ser Leu Val Ser Gly						
	250		255		260	
cac ggg aga gaa aat aaa agc tgc aga ggt tgg ggg tgg ggt cag gga	931					
His Gly Arg Glu Asn Lys Ser Cys Arg Gly Trp Gly Trp Gly Gln Gly						
	265		270		275	
ttc taggggatggg gcagagtgcc agcatc	960					
phe						

<210> 46

<211> 279

<212> PRT

<213> Homo sapiens

<400> 46

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20 25 30
Ser Val Glu Trp Glu Gly Arg Ser Leu Leu Lys Ala Leu Val Lys Lys
35 40 45
Ser Ala Leu Cys Gly Glu Gln Val His Ile Leu Gly Cys Glu Val Ser
50 55 60
Glu Glu Glu Phe Arg Glu Gly Phe Asp Ser Asp Ile Asn Asn Arg Leu
65 70 75 80
Val Tyr His Asp Phe Phe Arg Asp Pro Leu Asn Trp Ser Lys Thr Glu
85 90 95
Glu Ala Phe Pro Gly Gly Pro Leu Gly Ala Leu Arg Ala Met Cys Lys
100 105 110
Arg Thr Asp Pro Val Pro Val Thr Thr Ile Ala Leu Asp Ser Leu Ser Trp
115 120 125
Leu Leu Leu Arg Leu Pro Cys Thr Thr Leu Cys Gln Val Leu His Ala
130 135 140
Val Ser His Gln Asp Ser Cys Pro Gly Asp Ser Ser Val Gly Lys
145 150 155 160
Val Ser Val Leu Gly Leu Leu His Glu Glu Leu His Gly Pro Gly Pro
165 170 175
Val Gly Ala Leu Ser Ser Leu Ala Gln Thr Glu Val Thr Leu Gly Gly
180 185 190
Thr Met Gly Gln Ala Ser Ala His Ile Leu Cys Arg Arg Pro Arg Gln
195 200 205
Arg Pro Thr Asp Gln Thr Gln Trp Phe Ser Ile Leu Pro Asp Phe Ser
210 215 220
Leu Asp Leu Gln Glu Gly Pro Ser Val Glu Ser Gln Pro Tyr Ser Asp
225 230 235 240
Pro His Ile Pro Pro Val Ser Lys Asn Ala Lys Ala Arg Thr Arg Lys
245 250 255
Cys Ser Leu Val Ser Gly His Gly Arg Glu Asn Lys Ser Cys Arg Gly
260 265 270
Trp Gly Trp Gly Gln Gly Phe
275

<210> 47

<211> 1294

<212> DNA

<213> Homo sapiens

<220>

<221> 5'UTR

<222> 1..266

<220>

<221> CDS

<222> 267..1139

<220>

<221> 3'UTR

<222> 1140..1294

<220>

<221> polyA_signal

<222> 1246..1251

<220>

<221> polyA_site

<222> 1279..1294

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<400> 47
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aaattctttac ctcgctcttt cactgctagt aagatcagat tgcgtttctt tcagtttactc 120
ttcaatcgcc agttttcttga tctgcttcta aaagaagaag tagagaagat aaatcctgtc 180
ttcaatacct ggaaggaaaa acaaaataac ctcaactcgg ttttgaaaaa aacattccaa 240
gaactttcat cagagatttt acttag atg att tac aca atg aag aaa gta cat 293
Met Ile Tyr Thr Met Lys Lys Val His
-25 -20
gca ctt tgg gct tct gta tgc ctg ctg ctt aat ctt gcc cct gcc cct 341
Ala Leu Trp Ala Ser Val Cys Leu Leu Leu Asn Leu Ala Pro Ala Pro
-15 -10 -5
ctt aat gct gat tct gag gaa gat gaa gaa cac aca att atc aca gat 389
Leu Asn Ala Asp Ser Glu Glu Asp Glu Glu His Thr Ile Ile Thr Asp
1 5 10
acr gag ttg cca cca ctg aaa ctt atg cat tca ttt tgt gca ttc aag 437
Thr Glu Leu Pro Leu Lys Leu Met His Ser Phe Cys Ala Phe Lys
15 20 25 30
gcg gat gat ggc cca tgt aaa gca atc atg aaa aga ttt ttc ttc aat 485
Ala Asp Asp Gly Pro Cys Lys Ala Ile Met Lys Arg Phe Phe Phe Asn
35 40 45
att ttc act cga cag tgc gaa gaa ttt ata tat ggg gga tgt gaa gga 533
Ile Phe Thr Arg Gln Cys Glu Glu Phe Ile Tyr Gly Gly Cys Glu Gly
50 55 60
aat cag aat cga ttt gaa agt ctg gaa gag tgc aaa aaa atg tgt aca 581
Asn Gln Asn Arg Phe Glu Ser Leu Glu Glu Cys Lys Lys Met Cys Thr
65 70 75
aga gaa aag cca gat ttc tgc ttt ttg gaa gaa gat cct gga ata tgt 629
Arg Glu Lys Pro Asp Phe Cys Phe Leu Glu Glu Asp Pro Gly Ile Cys
80 85 90
cga ggt tat att acc agg tat ttt tat aac aat cag aca aaa cag tgt 677
Arg Gly Tyr Ile Thr Arg Tyr Phe Tyr Asn Gln Thr Lys Gln Cys
95 100 105 110
gaa cgt ttc aag tat ggt gga tgc ctg ggc aat atg aac aat ttt gag 725
Glu Arg Phe Lys Tyr Gly Gly Cys Leu Gly Asn Met Asn Asn Phe Glu
115 120 125
aca ctg gaa gaa tgc aag aac att tgt gaa gat ggt ccg aat ggt ttc 773
Thr Leu Glu Glu Cys Lys Asn Ile Cys Glu Asp Gly Pro Asn Gly Phe
130 135 140
cag gtg gat aat tat gga acc cag ctc aat gct gtg aat aac tcc ctg 821
Gln Val Asp Asn Tyr Gly Thr Gln Leu Asn Ala Val Asn Asn Ser Leu
145 150 155
act ccg caa tca acc aag gtt ccc agc ctt ttt gaa ttt cac ggt ccc 869
Thr Pro Gln Ser Thr Lys Val Pro Ser Leu Phe Glu Phe His Gly Pro
160 165 170
tca tgg tgt ctc act cca gca gac aga gga ttg tgt cgt gcc aat gag 917
Ser Trp Cys Leu Thr Pro Ala Asp Arg Gly Leu Cys Arg Ala Asn Glu
175 180 185 190
aac aga ttc tac tac aat tca gtc att ggg aaa tgc cgc cca ttt aag 965
Asn Arg Phe Tyr Thr Asn Ser Val Ile Gly Lys Cys Arg Pro Phe Lys
195 200 205
tac agt gga tgt ggg gga aat gaa aac aat ttt act tcc aaa caa gaa 1013
Tyr Ser Gly Cys Gly Gly Asn Glu Asn Asn Phe Thr Ser Lys Gln Glu
210 215 220
tgt ctg agg gca tgt aaa aaa ggt ttc atc caa aga ata tca aaa gga 1061
Cys Leu Arg Ala Cys Lys Lys Gly Phe Ile Gln Arg Ile Ser Lys Gly
225 230 235
ggc cta att aaa acc aaa aga aaa aga aag aag cag aga gtg aaa ata 1109
Gly Leu Ile Lys Thr Lys Arg Lys Arg Lys Lys Gln Arg Val Lys Ile
240 245 250
gca tat gaa gaa att ttt gtt aaa aat atg tgaattgtt atagcaatgt 1159
Ala Tyr Glu Glu Ile Phe Val Lys Asn Met

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<221> CDS
<222> 48..1100

<220>
<221> 3'UTR
<222> 1101..1194

<220>
<221> polyA_signal
<222> 1159..1164

<220>
<221> polyA_site
<222> 1179..1194

<400> 49
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Met Pro Ser
tct gtc tcg tgg ggc atc ctc ctg ctg gca ggc ctg tgc tgc ctg gtc 104
Ser Val Ser Trp Gly Ile Leu Leu Leu Ala Gly Leu Cys Cys Leu Val
-20 -15 -10 -5
cct gtc tcc ctg ggg acc aag gct gac act cac gat gaa atc ctg gag 152
Pro Val Ser Leu Gly Thr Lys Ala Asp Thr His Asp Glu Ile Leu Glu
1 5 10
ggc ctg aat ttc aac ctc acg gag att ccg gag gct cag atc cat gaa 200
Gly Leu Asn Phe Asn Leu Thr Glu Ile Pro Glu Ala Gln Ile His Glu
15 20 25
ggc ttc cag gaa ctc ctc cgt acc ctc aac cag cca gac agc cag ctc 248
Gly Phe Gln Glu Leu Leu Arg Thr Leu Asn Gln Pro Asp Ser Gln Leu
30 35 40
cag ctg acc acc ggc aat ggc ctg ttc ctc agc gag ggc ctg aag cta 296
Gln Leu Thr Thr Gly Asn Gly Leu Phe Leu Ser Glu Gly Leu Lys Leu
45 50 55 60
gtg gat aag ttt ttg gag gat gtt aaa aag ttg tac cac tca gaa gcc 344
Val Asp Lys Phe Leu Glu Asp Val Lys Lys Leu Tyr His Ser Glu Ala
65 70 75
ttc act gtc aac ttc ggg gac acc gaa gag gcc aag aaa cag atc aac 392
Phe Thr Val Asn Phe Gly Asp Thr Glu Glu Ala Lys Lys Gln Ile Asn
80 85 90
gat tac gtg gag aag ggt act caa ggg aaa att gtg gat ttg gtc aag 440
Asp Tyr Val Glu Lys Gly Thr Gln Gly Lys Ile Val Asp Leu Val Lys
95 100 105
gag ctt gac aga gac aca gtt ttt gct ctg gtg aat tac atc ttc ttt 488
Glu Leu Asp Arg Asp Thr Val Phe Ala Leu Val Asn Tyr Ile Phe Phe
110 115 120
aaa ggc aaa tgg gag aga ccc ttt gaa gtc aag gac acc gag gaa gag 536
Lys Gly Lys Trp Glu Arg Pro Phe Glu Val Lys Asp Thr Glu Glu Glu
125 130 135 140
gac ttc cac gtg gac cag gtg acc acc gtg aag gtg cct atg atg aag 584
Asp Phe His Val Asp Gln Val Thr Thr Val Lys Val Pro Met Met Lys
145 150 155
cgt tta ggc atg ttt aac atc cag cac tgt aag aag ctg tcc agc tgg 632
Arg Leu Gly Met Phe Asn Ile Gln His Cys Lys Lys Leu Ser Ser Trp
160 165 170
gtg ctg ctg atg aaa tac ctg ggc aat gcc acc gcc atc ttc ttc ctg 680
Val Leu Leu Met Lys Tyr Leu Gly Asn Ala Thr Ala Ile Phe Phe Leu
175 180 185
cct gat gag ggg aaa cta cag cac ctg gaa aat gaa ctc acc cac gat 728
Pro Asp Glu Gly Lys Leu Gln His Leu Glu Asn Glu Leu Thr His Asp
190 195 200
atc atc acc aag ttc ctg gaa aat gaa gac aga agg tct gcc agc tta 776
Ile Ile Thr Lys Phe Leu Glu Asn Glu Asp Arg Arg Ser Ala Ser Leu
205 210 215 220

cat tta ccc aaa ctg tcc att act gga acc tat gat ctg aag agc gtc	824
His Leu Pro Lys Leu Ser Ile Thr Gly Thr Tyr Asp Leu Lys Ser Val	
225 230 235	
ctg ggt caa ctg ggc atc act aag gtc ttc agc aat ggg gct gac ctc	872
Leu Gly Gln Leu Gly Ile Thr Lys Val Phe Ser Asn Gly Ala Asp Leu	
240 245 250	
tcc ggg gtc aca gag gag gca ccc ctg aag ctc tcc aag gcc gtg cat	920
Ser Gly Val Thr Glu Glu Ala Pro Leu Lys Leu Ser Lys Ala Val His	
255 260 265	
aag gct gtg ctg acc atc gac gag aaa ggg act gaa gct gct ggg gcc	968
Lys Ala Val Leu Thr Ile Asp Glu Lys Gly Thr Glu Ala Ala Gly Ala	
270 275 280	
atg ttt tta gag gcc ata ccc atg tct atc ccc ccc gag gtc aag ttc	1016
Met Phe Leu Glu Ala Ile Pro Met Ser Ile Pro Pro Glu Val Lys Phe	
285 290 295	
aac aaa ccc ttt gtc ttc tta atg att gac caa aat acc aag tct ccc	1064
Asn Lys Pro Phe Val Phe Leu Met Ile Asp Gln Asn Thr Lys Ser Pro	
305 310 315	
ctc ttc atg gga aaa gtg gtg aat ccc acc caa aaa taactgcctc	1110
Leu Phe Met Gly Lys Val Val Asn Pro Thr Gln Lys	
320 325	
tcgctctca acccctcccc tccatccctg gccccctccc tggatgacat taaagaagg	1170
ttgagctgaa aaaaaaaaaa aaaa	1194

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 -5 1 5
 Ile Leu Glu Gly Leu Asn Phe Asn Leu Thr Glu Ile Pro Glu Ala Gln
 10 15 20
 Ile His Glu Gly Phe Gln Glu Leu Leu Arg Thr Leu Asn Gln Pro Asp
 25 30 35 40
 Ser Gln Leu Gln Leu Thr Thr Gly Asn Gly Leu Phe Leu Ser Glu Gly
 45 50 55
 Leu Lys Leu Val Asp Lys Phe Leu Glu Asp Val Lys Lys Leu Tyr His
 60 65 70
 Ser Glu Ala Phe Thr Val Asn Phe Gly Asp Thr Glu Glu Ala Lys Lys
 75 80 85
 Gln Ile Asn Asp Tyr Val Glu Lys Gly Thr Gln Gly Lys Ile Val Asp
 90 95 100
 Leu Val Lys Glu Leu Asp Arg Asp Thr Val Phe Ala Leu Val Asn Tyr
 105 110 115 120
 Ile Phe Phe Lys Gly Lys Trp Glu Arg Pro Phe Glu Val Lys Asp Thr
 125 130 135
 Glu Glu Glu Asp Phe His Val Asp Gln Val Thr Thr Val Lys Val Pro
 140 145 150
 Met Met Lys Arg Leu Gly Met Phe Asn Ile Gln His Cys Lys Lys Leu
 155 160 165
 Ser Ser Trp Val Leu Leu Met Lys Tyr Leu Gly Asn Ala Thr Ala Ile
 170 175 180
 Phe Phe Leu Pro Asp Glu Gly Lys Leu Gln His Leu Glu Asn Glu Leu
 185 190 195 200
 Thr His Asp Ile Ile Thr Lys Phe Leu Glu Asn Glu Asp Arg Arg Ser

205										210										215																											
Ala	Ser	Leu	His	Leu	Pro	Lys	Leu	Ser	Ile	Thr	Gly	Thr	Tyr	Asp	Leu	Ala	Ser	Leu	His	Leu	Pro	Lys	Leu	Ser	Ile	Thr	Gly	Thr	Tyr	Asp	Leu	Ala	Ser	Leu	His	Leu	Pro	Lys	Leu	Ser	Ile	Thr	Gly	Thr	Tyr	Asp	Leu
220										225										230																											
Lys	Ser	Val	Leu	Gly	Gln	Leu	Gly	Ile	Thr	Lys	Val	Phe	Ser	Asn	Gly	Lys	Ser	Val	Leu	Gly	Gln	Leu	Gly	Ile	Thr	Lys	Val	Phe	Ser	Asn	Gly	Lys	Ser	Val	Leu	Gly	Gln	Leu	Gly	Ile	Thr	Lys	Val	Phe	Ser	Asn	Gly
235										240										245																											
Ala	Asp	Leu	Ser	Gly	Val	Thr	Glu	Glu	Ala	Pro	Leu	Lys	Leu	Ser	Lys	Ala	Asp	Leu	Ser	Gly	Val	Thr	Glu	Glu	Ala	Pro	Leu	Lys	Leu	Ser	Lys	Ala	Asp	Leu	Ser	Gly	Val	Thr	Glu	Glu	Ala	Pro	Leu	Lys	Leu	Ser	Lys
250										255										260																											
Ala	Val	His	Lys	Ala	Val	Leu	Thr	Ile	Asp	Glu	Lys	Gly	Thr	Glu	Ala	Ala	Val	His	Lys	Ala	Val	Leu	Thr	Ile	Asp	Glu	Lys	Gly	Thr	Glu	Ala	Ala	Val	His	Lys	Ala	Val	Leu	Thr	Ile	Asp	Glu	Lys	Gly	Thr	Glu	Ala
265										270										275																											
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285										290										295																											
Val	Lys	Phe	Asn	Lys	Pro	Phe	Val	Phe	Leu	Met	Ile	Asp	Gln	Asn	Thr	Val	Lys	Phe	Asn	Lys	Pro	Phe	Val	Phe	Leu	Met	Ile	Asp	Gln	Asn	Thr	Val	Lys	Phe	Asn	Lys	Pro	Phe	Val	Phe	Leu	Met	Ile	Asp	Gln	Asn	Thr
300										305										310																											
Lys	Ser	Pro	Leu	Phe	Met	Gly	Lys	Val	Val	Asn	Pro	Thr	Gln	Lys	Lys	Ser	Pro	Leu	Phe	Met	Gly	Lys	Val	Val	Asn	Pro	Thr	Gln	Lys	Lys	Ser	Pro	Leu	Phe	Met	Gly	Lys	Val	Val	Asn	Pro	Thr	Gln	Lys			
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<220>
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 <222> 1269..1274

<220>
 <221> polyA_site
 <222> 1302..1317

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 cgacttttagg ctggataata gtcaaatctt tacctcgctc ttctactgct agtaagatca 120
 gattgcgttt ctttcagtta ctcttcaatc gccagtttct tgatctgctt ctaaaagaag 180
 aagtagagaa gataaatcct gtcttcaata cctggaagga aaaaacaaat aaactcaact 240
 ccgttttgaa aaaaacattc caagaacttt catcagagat ttactttag atg att tac 298
 Met Ile Tyr
 -25
 aca atg aag aaa gta cat gca ctt tgg gct tct gta tgc ctg ctg ctt 346
 Thr Met Lys Lys Val His Ala Leu Trp Ala Ser Val Cys Leu Leu Leu
 -20 -15 -10
 aat ctt gcc cct gcc cct ctt aat gct gat tct gag gaa gat gaa gaa 394
 Asn Leu Ala Pro Ala Pro Leu Asn Ala Asp Ser Glu Glu Asp Glu Glu
 -5 1 5
 cac aca att atc aca gat acg gag ttg cca cca ctg aaa ctt atg cat 442
 His Thr Ile Ile Thr Asp Thr Glu Leu Pro Pro Leu Lys Leu Met His
 10 15 20
 tca ttt tgt gca ttc aag tgc gat gat ggc cca tgt aaa gca atc atg 490
 Ser Phe Cys Ala Phe Lys Ser Asp Asp Gly Pro Cys Lys Ala Ile Met
 25 30 35 40
 aaa aga ttt ttc ttc aat att ttc act cga cag tgc gaa gaa ttt ata 538
 Lys Arg Phe Phe Phe Asn Ile Phe Thr Arg Gln Cys Glu Glu Phe Ile

	45	50	55	
tat ggg gga tgt gaa gga aat cag aat cga ttt gaa agt ctg gaa gag				586
Tyr Gly Gly Cys Glu Gly Asn Gln Asn Arg Phe Glu Ser Leu Glu Glu				
	60	65	70	
tgc aaa aaa atg tgt aca aga gaa aag cca gat ttc tgc ttt ttg gaa				634
Cys Lys Lys Met Cys Thr Arg Glu Lys Pro Asp Phe Cys Phe Leu Glu				
	75	80	85	
gaa gat cct gga ata tgt cga ggt tat att acc agg tat ttt tat aac				682
Glu Asp Pro Gly Ile Cys Arg Gly Tyr Ile Thr Arg Tyr Phe Tyr Asn				
	90	95	100	
aat cag aca aaa cag tgt gaa cgt ttc aag tat ggt gga tgc ctg ggc				730
Asn Gln Thr Lys Gln Cys Glu Arg Phe Lys Tyr Gly Gly Cys Leu Gly				
	105	110	115	
aat atg aac aat ttt gag aca ctg gaa gaa tgc aag aac att tgt gaa				778
Asn Met Asn Asn Phe Glu Thr Leu Glu Glu Cys Lys Asn Ile Cys Glu				
	125	130	135	
gat ggt ccg aat ggt ttc cag gtg gat aat tat gga acc cag ctg aat				826
Asp Gly Pro Asn Gly Phe Gln Val Asp Asn Tyr Gly Thr Gln Leu Asn				
	140	145	150	
gct gtg aat aac tcc ctg act ccg caa tca acc aag gtt ccc agc ctt				874
Ala Val Asn Asn Ser Leu Thr Pro Gln Ser Thr Lys Val Pro Ser Leu				
	155	160	165	
ttt gaa ttt cac ggt ccc tca tgg tgt ctg act cca gca gac aga gga				922
Phe Glu Phe His Gly Pro Ser Trp Cys Leu Thr Pro Ala Asp Arg Gly				
	170	175	180	
ttg tgt cgt gcc aat gag aac aga ttc tac tac aat tca gtc att ggg				970
Leu Cys Arg Ala Asn Glu Asn Arg Phe Tyr Tyr Asn Ser Val Ile Gly				
	185	190	195	
aaa tgc cgc cca ttt aag tac agt gga tgt ggg gga aat gaa aac aat				1018
Lys Cys Arg Pro Phe Lys Tyr Ser Gly Cys Gly Gly Asn Glu Asn Asn				
	205	210	215	
ttt act tcc aaa caa gaa tgt ctg agg gca tgt aaa aaa ggt ttc atc				1066
Phe Thr Ser Lys Gln Glu Cys Leu Arg Ala Cys Lys Lys Gly Phe Ile				
	220	225	230	
caa aga ata tca aaa gga ggc cta att aaa acc aaa aga aag aag				1114
Gln Arg Ile Ser Lys Gly Gly Leu Ile Lys Thr Lys Arg Lys Arg Lys				
	235	240	245	
aag cag aga gtg aaa ata gca tat gaa gaa att ttt gtt aaa aat atg				1162
Lys Gln Arg Val Lys Ile Ala Tyr Glu Glu Ile Phe Val Lys Asn Met				
	250	255	260	
tgaattgttt atagcaatgt aacattaatt ctactaaata ttttatatga aatgtttcac				1222
tatgatttct tatttttctt ctaaaatgct tttaattaat atgttccatta aattttctat				1282
gcttattgta cttgttatca aaaaaaaaaa aaaaaa				1317

<210> 52
 <211> 291
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..28

<400> 52
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 -10 -5 1
 Asp Glu Glu His Thr Ile Ile Thr Asp Thr Glu Leu Pro Pro Leu Lys
 5 10 15 20
 Leu Met His Ser Phe Cys Ala Phe Lys Ser Asp Asp Gly Pro Cys Lys
 25 30 35
 Ala Ile Met Lys Arg Phe Phe Phe Asn Ile Phe Thr Arg Gln Cys Glu

1 5 10 15
 Ala Ala His Cys Leu Glu Lys Ser Pro Arg Pro Ser Ser Tyr Lys Val
 20 25 30
 Ile Leu Gly Ala His Gln Glu Val Asn Leu Glu Pro His Val Gln Glu
 35 40 45
 Ile Glu Val Ser Arg Leu Phe Leu Glu Pro Thr Arg Lys Asp Ile Ala
 50 55 60
 Leu Leu Lys Leu Ser Ser Pro Ala Val Ile Thr Asp Lys Val Ile Pro
 65 70 75 80
 Ala Cys Leu Pro Ser Pro Asn Tyr Val Val Ala Asp Arg Thr Glu Cys
 85 90 95
 Phe Ile Thr Gly Trp Gly Glu Thr Gln Gly Thr Phe Gly Ala Gly Leu
 100 105 110
 Leu Lys Glu Ala Gln Leu Pro Val Ile Glu Asn Lys Val Cys Asn Arg
 115 120 125
 Tyr Glu Phe Leu Asn Gly Arg Val Gln Ser Thr Glu Leu Cys Ala Gly
 130 135 140
 His Leu Ala Gly Gly Thr Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro
 145 150 155 160
 Leu Val Cys Phe Glu Lys Asp Lys Tyr Ile Leu Gln Gly Val Thr Ser
 165 170 175
 Trp Gly Leu Gly Cys Ala Arg Pro Asn Lys Pro Gly Val Tyr Val Arg
 180 185 190
 Val Ser Arg Phe Val Thr Trp Ile Glu Gly Val Met Arg Asn Asn
 195 200 205

<210> 55
 <211> 809
 <212> DNA
 <213> Homo sapiens

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 <221> CDS
 <222> 26..628

<220>
 <221> 3'UTR
 <222> 629..809

<220>
 <221> polyA_signal
 <222> 766..771

<220>
 <221> polyA_site
 <222> 795..809

<400> 55
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 1 Met Leu Glu Val Ser Asp Ala Leu Gly
 gga cct gga aga gta cca ggg gcc aca gca ggg atg aat gga gtg gac 100
 Gly Pro Gly Arg Val Pro Gly Ala Thr Ala Gly Met Asn Gly Val Asp
 10 15 20 25
 acg tcg ctt ctc tgt gat ttg ttg cag gcc ctg acc ttc ctg acc aga 148
 Thr Ser Leu Leu Cys Asp Leu Leu Gln Ala Leu Thr Phe Leu Thr Arg
 30 35 40
 aat gaa att ctg tgc atc cat gac acc ttc ctg aag ctc tgc cct cct 196
 Asn Glu Ile Leu Cys Ile His Asp Thr Phe Leu Lys Leu Cys Pro Pro

[illegible]

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<210> 56
<211> 201
<212> PRT
<213> Homo sapiens
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			20					25					30		
Leu	Gln	Ala	Leu	Thr	Phe	Leu	Thr	Arg	Asn	Glu	Ile	Leu	Cys	Ile	His
			35				40					45			
Asp	Thr	Phe	Leu	Lys	Leu	Cys	Pro	Pro	Gly	Lys	Tyr	Tyr	Lys	Glu	Ala
	50					55				60					
Thr	Leu	Thr	Met	Asp	Gln	Val	Ser	Ser	Leu	Pro	Ala	Leu	Arg	Val	Asn
65					70					75				80	
Pro	Phe	Arg	Asp	Arg	Ile	Cys	Arg	Val	Phe	Ser	His	Lys	Gly	Met	Phe
				85					90					95	
Ser	Phe	Glu	Asp	Val	Leu	Gly	Met	Ala	Ser	Val	Phe	Ser	Glu	Gln	Ala
			100					105					110		
Cys	Pro	Ser	Leu	Lys	Ile	Glu	Tyr	Ala	Phe	Arg	Ile	Tyr	Asp	Phe	Asn
			115				120					125			
Glu	Asn	Gly	Phe	Ile	Asp	Glu	Glu	Asp	Leu	Gln	Arg	Ile	Ile	Leu	Arg
			130			135					140				
Leu	Leu	Asn	Ser	Asp	Asp	Met	Ser	Glu	Asp	Leu	Leu	Met	Asp	Leu	Thr
145					150					155				160	
Asn	His	Val	Leu	Ser	Glu	Ser	Asp	Leu	Asp	Asn	Asp	Asn	Met	Leu	Ser
				165					170					175	
Phe	Ser	Glu	Phe	Glu	His	Ala	Met	Ala	Lys	Ser	Pro	Asp	Phe	Met	Asn
			180					185					190		

Ser Phe Arg Ile His Phe Trp Gly Cys
195 200

<210> 57
<211> 1133
<212> DNA
<213> Homo sapiens

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<222> 476..964

<220>
<221> 3'UTR
<222> 965..1133

<220>
<221> polyA_signal
<222> 1101..1106

<220>
<221> polyA_site
<222> 1118..1133

<400> 57
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gagccaggag gtggcaggac gaggtaggag gctggttcag tagctcgggc aagagcaggg 120
ccccccagga tctgaaggcc tcccaggccc cccaggccca ggggttccca gaggagagcg 180
aggacccccaa ggtaactccg gtgagaaggg cgaccaggga tttaaggcc agccaggctt 240
tcggggccca ccgggtcccc ctggattccc agggcaaaagt ggatcacctg gccacactgg 300
ccctcaagca gagaaggcca gcgaagggat tcgaggccca tcaggcctgc ctggctcccc 360
tgggccaccg ggacctctcg ggattcaggg cccgcgggt ctggatgggt tggatgggaa 420
ggatggcaag cctggcttga ggggggaccc tggtcctgct ggcacctg gactc atg 478

Met
1

gga cca ccg ggc ttt aag ggg aaa aca gga cat cct ggc ctc cca gga 526
Gly Pro Pro Gly Phe Lys Gly Lys Thr Gly His Pro Gly Leu Pro Gly
5 10 15
cct aag ggt gac tgt ggc aaa cca ggt cct cct ggc agc act ggc cgg 574
Pro Lys Gly Asp Cys Gly Lys Pro Gly Pro Pro Gly Ser Thr Gly Arg
20 25 30
cct ggc gca gag ggt gaa cct ggt gcc atg gga ccc cag gga aga ccc 622
Pro Gly Ala Glu Gly Glu Pro Gly Ala Met Gly Pro Gln Gly Arg Pro
35 40 45
ggt ccc ccg gga cac gtt ggg cca cca ggg cct cca ggc cag cca gga 670
Gly Pro Pro Gly His Val Gly Pro Pro Gly Pro Pro Gly Gln Pro Gly
50 55 60 65
cca gct ggg atc tct gca gtg ggt ctg aaa gga gac cga gga gcc acc 718
Pro Ala Gly Ile Ser Ala Val Gly Leu Lys Gly Asp Arg Gly Ala Thr
70 75 80
gga gaa agg ggc ctt gca ggc ctc cca ggc cag ccc ggc ccc cca ggt 766
Gly Glu Arg Gly Leu Ala Gly Leu Pro Gly Gln Pro Gly Pro Pro Gly
85 90 95
cct caa ggt cct cca ggc tat ggc aag atg ggt gca aca gga cca atg 814
Pro Gln Gly Pro Pro Gly Tyr Gly Lys Met Gly Ala Thr Gly Pro Met
100 105 110
ggc cag caa ggc atc cct ggc atc cct ggg ccc ccg ggt ccc atg ggc 862
Gly Gln Gln Gly Ile Pro Gly Ile Pro Gly Pro Pro Gly Pro Met Gly
115 120 125

cag cca ggc aag gct ggc cac tgt aat ccc tct gac tgc ttt ggg gcc 910
 Gln Pro Gly Lys Ala Gly His Cys Asn Pro Ser Asp Cys Phe Gly Ala
 130 135 140 145
 atg ccg atg gag cag cag tac cca ccc atg aaa acc atg aag ggg cct 958
 Met Pro Met Glu Gln Gln Tyr Pro Pro Met Lys Thr Met Lys Gly Pro
 150 155 160
 ttt ggc tgaattccc cacctgcctt tggatgaaag actccgttgg gaataaatgg 1014
 Phe Gly
 ccaaagctta taggactctg tgacaggttg tgaatgtttt tttgttgttt gttgtgtgtt 1074
 ttaattgctg ttaatatattt ttaataata aagaacaaaa actaaaaaaaa aaaaaaaaaa 1133

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 <211> 163
 <212> PRT
 <213> Homo sapiens

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 Arg Pro Gly Ala Glu Gly Glu Pro Gly Ala Met Gly Pro Gln Gly Arg
 35 40 45
 Pro Gly Pro Pro Gly His Val Gly Pro Pro Gly Pro Gly Gln Pro
 50 55 60
 Gly Pro Ala Gly Ile Ser Ala Val Gly Leu Lys Gly Asp Arg Gly Ala
 65 70 75 80
 Thr Gly Glu Arg Gly Leu Ala Gly Leu Pro Gly Gln Pro Gly Pro Pro
 85 90 95
 Gly Pro Gln Gly Pro Pro Gly Tyr Gly Lys Met Gly Ala Thr Gly Pro
 100 105 110
 Met Gly Gln Gln Gly Ile Pro Gly Ile Pro Gly Pro Gly Pro Met
 115 120 125
 Gly Gln Pro Gly Lys Ala Gly His Cys Asn Pro Ser Asp Cys Phe Gly
 130 135 140
 Ala Met Pro Met Glu Gln Gln Tyr Pro Pro Met Lys Thr Met Lys Gly
 145 150 155 160
 Pro Phe Gly

<210> 59
 <211> 838
 <212> DNA
 <213> Homo sapiens

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 <222> 79..642

<220>
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 <222> 643..838

<220>
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 <222> 799..804

<220>
 <221> polyA_site
 <222> 823..838

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cttgaacttt tggccgcc atg tgc ttc ccg aag gtc ctc tct gat gac atg 111
Met Cys Phe Pro Lys Val Leu Ser Asp Asp Met
1 5 10
aag aag ctg aag gcc cga atg cac cag gcc ata gaa aga ttt tat gat 159
Lys Lys Leu Lys Ala Arg Met His Gln Ala Ile Glu Arg Phe Tyr Asp
15 20 25
aaa atg caa aat gca gaa tca gga cgt gga cag gtg atg tgc agc ctg 207
Lys Met Gln Asn Ala Glu Ser Gly Arg Gly Gln Val Met Ser Ser Leu
30 35 40
gca gag ctg gag gac gac ttc aaa gag ggc tac ctg gag aca gtg gcg 255
Ala Glu Leu Glu Asp Asp Phe Lys Glu Gly Tyr Leu Glu Thr Val Ala
45 50 55
gct tat tat gag gag cag cac cca gag ctc act cct cta ctt gaa aaa 303
Ala Tyr Tyr Glu Glu Gln His Pro Glu Leu Thr Pro Leu Leu Glu Lys
60 65 70 75
gaa aga gat gga tta cgg tgc cga ggc aac aga tcc cct gtc ccg gat 351
Glu Arg Asp Gly Leu Arg Cys Arg Gly Asn Arg Ser Pro Val Pro Asp
80 85 90
gtt gag gat ccc gca acc gag gag cct ggg gag agc ttt tgt gac aag 399
Val Glu Asp Pro Ala Thr Glu Glu Pro Gly Glu Ser Phe Cys Asp Lys
95 100 105
gtc atg aga tgg ttc cag gcc atg ctg cag cgg ctg cag acc tgg tgg 447
Val Met Arg Trp Phe Gln Ala Met Leu Gln Arg Leu Gln Thr Trp Trp
110 115 120
cac ggg gtt ctg gcc tgg gtg aag gag aag gtg gtg gcc ctg gtc cat 495
His Gly Val Leu Ala Trp Val Lys Glu Lys Val Val Ala Leu Val His
125 130 135
gca gtg cag gcc ctc tgg aaa cag ttc cag agt ttc tgc tgc tct ctg 543
Ala Val Gln Ala Leu Trp Lys Gln Phe Gln Ser Phe Cys Cys Ser Leu
140 145 150 155
tca gag ctc ttc atg tcc tct ttc cag tcc tac gga gcc cca cgg ggg 591
Ser Glu Leu Phe Met Ser Ser Phe Gln Ser Tyr Gly Ala Pro Arg Gly
160 165 170
gac aag gag gag ctg aca ccc cag aag tgc tct gaa ccc caa tcc tca 639
Asp Lys Glu Glu Leu Thr Pro Gln Lys Cys Ser Glu Pro Gln Ser Ser
175 180 185
aaa tgaagatact gacaccacct ttgcctccc cgtaccgcg caccacctt 692
Lys
gacctctccc tcagctgtcc tgtgccccgc cctctccgc acactcagtc cccctgcctg 752
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<211> 188

<212> PRT

<213> Homo sapiens

<400> 60

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20 25 30
Glu Ser Gly Arg Gly Gln Val Met Ser Ser Leu Ala Glu Leu Glu Asp
35 40 45
Asp Phe Lys Glu Gly Tyr Leu Glu Thr Val Ala Ala Tyr Tyr Glu Glu
50 55 60
Gln His Pro Glu Leu Thr Pro Leu Leu Glu Lys Glu Arg Asp Gly Leu
65 70 75 80
Arg Cys Arg Gly Asn Arg Ser Pro Val Pro Asp Val Glu Asp Pro Ala
85 90 95

Thr Glu Glu Pro Gly Glu Ser Phe Cys Asp Lys Val Met Arg Trp Phe
 100 105 110
 Gln Ala Met Leu Gln Arg Leu Gln Thr Trp Trp His Gly Val Leu Ala
 115 120 125
 Trp Val Lys Glu Lys Val Val Ala Leu Val His Ala Val Gln Ala Leu
 130 135 140
 Trp Lys Gln Phe Gln Ser Phe Cys Cys Ser Leu Ser Glu Leu Phe Met
 145 150 155 160
 Ser Ser Phe Gln Ser Tyr Gly Ala Pro Arg Gly Asp Lys Glu Glu Leu
 165 170 175
 Thr Pro Gln Lys Cys Ser Glu Pro Gln Ser Ser Lys
 180 185

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 <212> DNA
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<220>
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 <222> 159..764

<220>
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 <222> 765..862

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 ttgctgtgtc ctttaagact gcagcctggg cctgggtgt cactgcgttc ggaccagac 120
 ccgtgcaggc cagcagcagc ccccgccgc gcagcagc atg gag ctc tgg ggg gcc 176
 Met Glu Leu Trp Gly Ala
 -20 -15
 tac ctc ctc ctc tgc ctc ttc tcc ctc ctg acc cag gtc acc acc gag 224
 Tyr Leu Leu Leu Cys Leu Phe Ser Leu Leu Thr Thr Thr Glu
 -10 -5 1
 cca cca acc cag aag ccc aag aag att gta aat gcc aag aaa gat gtt 272
 Pro Pro Thr Gln Lys Pro Lys Lys Ile Val Asn Ala Lys Lys Asp Val
 5 10 15
 gtg aac aca aag atg ttt gag gag ctc aag agc cgt ctg gac acc ctg 320
 Val Asn Thr Lys Met Phe Glu Glu Leu Lys Ser Arg Leu Asp Thr Leu
 20 25 30
 gcc cag gag gtg gcc ctg ctg aag gag cag cag gcc ctg cag acg gtc 368
 Ala Gln Glu Val Ala Leu Leu Lys Glu Gln Gln Ala Leu Gln Thr Val
 35 40 45 50
 tgc ctg aag ggg acc aag gtg cac atg aaa tgc ttt ctg gcc ttc acc 416
 Cys Leu Lys Gly Thr Lys Val His Met Lys Cys Phe Leu Ala Phe Thr
 55 60 65
 cag acg aag acc ttc cac gag tcc agc gag gac tgc atc tgc cgc ggg 464
 Gln Thr Lys Thr Phe His Glu Ser Ser Glu Asp Cys Ile Ser Arg Gly
 70 75 80
 ggc acc ctg agc acc cct cag act ggc tgc gag aac gac gcc ctg tat 512
 Gly Thr Leu Ser Thr Pro Gln Thr Gly Ser Glu Asn Asp Ala Leu Tyr
 85 90 95
 gag tac ctg cgc cag agc gtg gcc aac gag gcc gag atc tgg ctg ggc 560
 Glu Tyr Leu Arg Gln Ser Val Gly Asn Glu Ala Glu Ile Trp Leu Gly
 100 105 110
 ctc aac gac atg ggc gcc gag ggc acc tgg gtg gac atg acc ggc gcc 608
 Leu Asn Asp Met Ala Ala Glu Gly Thr Trp Val Asp Met Thr Gly Ala
 115 120 125 130

cgc atc gcc tac aag aac tgg gag act gag atc acc gcg caa ccc gat 656
 Arg Ile Ala Tyr Lys Asn Trp Glu Thr Glu Ile Thr Ala Gln Pro Asp
 135 140 145
 ggc ggc aag acc gag aac tgc gcg gtc ctg tca ggc gcg gcc aac ggc 704
 Gly Gly Lys Thr Glu Asn Cys Ala Val Leu Ser Gly Ala Ala Asn Gly
 150 155 160
 aag tgg ttc gac aag cgc tgc cgc gat cag ctg ccc tac atc tgc cag 752
 Lys Trp Phe Asp Lys Arg Cys Arg Asp Gln Leu Pro Tyr Ile Cys Gln
 165 170 175
 ttc ggc atc gtg tagccggcgg ggccggggccc gtggggggccc tggaggagg 804
 Phe Gly Ile Val
 180
 caggagccgc gggaggccgg gaggagggtg gggaccttgc agcccccatc ctctccgt 862

<210> 62
 <211> 202
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..21

<400> 62
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 Thr Gln Val Thr Thr Glu Pro Pro Thr Gln Lys Pro Lys Lys Ile Val
 -5 1 5 10
 Asn Ala Lys Lys Asp Val Val Asn Thr Lys Met Phe Glu Glu Leu Lys
 15 20 25
 Ser Arg Leu Asp Thr Leu Ala Gln Glu Val Ala Leu Leu Lys Glu Gln
 30 35 40
 Gln Ala Leu Gln Thr Val Cys Leu Lys Gly Thr Lys Val His Met Lys
 45 50 55
 Cys Phe Leu Ala Phe Thr Gln Thr Lys Thr Phe His Glu Ser Ser Glu
 60 65 70 75
 Asp Cys Ile Ser Arg Gly Gly Thr Leu Ser Thr Pro Gln Thr Gly Ser
 80 85 90
 Glu Asn Asp Ala Leu Tyr Glu Tyr Leu Arg Gln Ser Val Gly Asn Glu
 95 100 105
 Ala Glu Ile Trp Leu Gly Leu Asn Asp Met Ala Ala Glu Gly Thr Trp
 110 115 120
 Val Asp Met Thr Gly Ala Arg Ile Ala Tyr Lys Asn Trp Glu Thr Glu
 125 130 135
 Ile Thr Ala Gln Pro Asp Gly Gly Lys Thr Glu Asn Cys Ala Val Leu
 140 145 150 155
 Ser Gly Ala Ala Asn Gly Lys Trp Phe Asp Lys Arg Cys Arg Asp Gln
 160 165 170
 Leu Pro Tyr Ile Cys Gln Phe Gly Ile Val
 175 180

<210> 63
 <211> 618
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 1..194

<220>
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 <222> 195..587

<220>
 <221> 3'UTR
 <222> 588..618

<220>
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 <222> 578..583

<220>
 <221> polyA_site
 <222> 604..618

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 cctacaaggg cctccctgac acccaagttc atattgctca gaaacagtga acttgagttt 120
 ttcgttttac cttgatctct ccttgacaaa gaaatccaga tgatgcgaga cctgatgaag 180
 acaatacatg gaaa atg aca gtc ttg gaa ata act ttg gct gtc atc ctg 230
 Met Thr Val Leu Glu Ile Thr Leu Ala Val Ile Leu
 -20 -15 -10
 act cta ctg gga ctt gcc atc ctg gct att ttg tta aca aga tgg gca 278
 Thr Leu Leu Gly Leu Ala Ile Leu Ala Ile Leu Thr Arg Trp Ala
 -5 1 5
 cga cgt aag caa agt gaa atg cat atc tcc aga tac agt tca gaa caa 326
 Arg Arg Lys Gln Ser Glu Met His Ile Ser Arg Tyr Ser Ser Glu Gln
 10 15 20
 agt gct aga ctt ctg gac tat gag gat ggt aga gga tcc cga cat gca 374
 Ser Ala Arg Leu Leu Asp Tyr Glu Asp Gly Arg Gly Ser Arg His Ala
 25 30 35
 tat tca aca caa agt gag aga tcc aaa aga gat tac aca cca tca acc 422
 Tyr Ser Thr Gln Ser Glu Arg Ser Lys Arg Asp Tyr Thr Pro Ser Thr
 40 45 50 55
 aac tct cta gca ctg tct cga tca agt att gct tta cct caa gga tcc 470
 Asn Ser Leu Ala Leu Ser Arg Ser Ser Ile Ala Leu Pro Gln Gly Ser
 60 65 70
 atg agt agt ata aaa tgt tta caa aca act gaa gaa ctt cct tcc aga 518
 Met Ser Ser Ile Lys Cys Leu Gln Thr Thr Glu Glu Leu Pro Ser Arg
 75 80 85
 act gca gga gcc atg agt aag ttc ttt ttc tgc cct tta att ctc atg 566
 Thr Ala Gly Ala Met Ser Lys Phe Phe Phe Cys Pro Leu Ile Leu Met
 90 95 100
 tgc ttt gct tta cta aac tgt tagaatatgt aagacgaaaa aaaaaaaaaa a 618
 Cys Phe Ala Leu Leu Asn Cys
 105 110

<210> 64
 <211> 131
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..22

<400> 64
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 -20 -15 -10
 Leu Ala Ile Leu Ala Ile Leu Leu Thr Arg Trp Ala Arg Arg Lys Gln
 -5 1 5 10
 Ser Glu Met His Ile Ser Arg Tyr Ser Ser Glu Gln Ser Ala Arg Leu
 15 20 25
 Leu Asp Tyr Glu Asp Gly Arg Gly Ser Arg His Ala Tyr Ser Thr Gln
 30 35 40

Ser Glu Arg Ser Lys Arg Asp Tyr Thr Pro Ser Thr Asn Ser Leu Ala
 45 50 55
 Leu Ser Arg Ser Ser Ile Ala Leu Pro Gln Gly Ser Met Ser Ser Ile
 60 65 70
 Lys Cys Leu Gln Thr Thr Glu Glu Leu Pro Ser Arg Thr Ala Gly Ala
 75 80 85 90
 Met Ser Lys Phe Phe Phe Cys Pro Leu Ile Leu Met Cys Phe Ala Leu
 95 100 105
 Leu Asn Cys

<210> 65
 <211> 836
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..176

<220>
 <221> CDS
 <222> 177..767

<220>
 <221> 3'UTR
 <222> 768..836

<220>
 <221> polyA_signal
 <222> 814..819

<220>
 <221> polyA_site
 <222> 822..836

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 acacccaagt tcatattgct cagaaacagt gaacttgagt ttttcatttt accttgatct 120
 ctctctgaca aagaaatcca gatgatgcca gacctgatga agacaatata tggaaa atg 179
 Met
 aca gtc ttg gaa ata act ttg gct gtc atc ctg act cta ctg gga ctt 227
 Thr Val Leu Glu Ile Thr Leu Ala Val Ile Leu Thr Leu Gly Leu
 -20 -15 -10 -5
 gcc atc ctg gct att ttg tta aca aga tgg gca cga cgt aag caa agt 275
 Ala Ile Leu Ala Ile Leu Leu Thr Arg Trp Ala Arg Arg Lys Gln Ser
 1 5 10
 gaa atg tat atc tcc aga tac agt tca gaa caa agt gct aga ctt ctg 323
 Glu Met Tyr Ile Ser Arg Tyr Ser Ser Glu Gln Ser Ala Arg Leu Leu
 15 20 25
 gac tat gag gat ggt aga gga tcc cga cat gca tat tca aca caa agt 371
 Asp Tyr Glu Asp Gly Arg Gly Ser Arg His Ala Tyr Ser Thr Gln Ser
 30 35 40
 gag aga tcc aaa aga gat tac aca cca tca acc aac tct cta gca ctg 419
 Glu Arg Ser Lys Arg Asp Tyr Thr Pro Ser Thr Asn Ser Leu Ala Leu
 45 50 55 60
 tct cga tca agt att gct tta cct caa gga tcc atg agt agt ata aaa 467
 Ser Arg Ser Ser Ile Ala Leu Pro Gln Gly Ser Met Ser Ser Ile Lys
 65 70 75
 tgt tta caa aca act gaa gaa cct cct tcc aga act gca gga gcc atg 515
 Cys Leu Gln Thr Thr Glu Glu Pro Pro Ser Arg Thr Ala Gly Ala Met
 80 85 90
 atg caa ttc aca gcc cct att ccc gga gct aca gga cct atc aag ctc 563
 Met Gln Phe Thr Ala Pro Ile Pro Gly Ala Thr Gly Pro Ile Lys Leu

95 100 105
 tct caa aaa acc att gtg caa act cta gga cct att gta caa tat cct 611
 Ser Gln Lys Thr Ile Val Gln Thr Leu Gly Pro Ile Val Gln Tyr Pro
 110 115 120
 gga tcc aat ggg agg ata aac ata agc cag ctc acc tca gag gat ctc 659
 Gly Ser Asn Gly Arg Ile Asn Ile Ser Gln Leu Thr Ser Glu Asp Leu
 125 130 135 140
 act ggg gct aaa gga agg gtc aca tct ggt cca cag ttc cct aat agc 707
 Thr Gly Ala Lys Gly Arg Val Thr Ser Gly Pro Gln Phe Pro Asn Ser
 145 150 155
 cac cat gtg cca gag aat cta cat gga tac atg aat tcc ctt tcc ctt 755
 His His Val Pro Glu Asn Leu His Gly Tyr Met Asn Ser Leu Ser Leu
 160 165 170
 ttc tcc cct gct tgactccctc tcccttatgt gtaacaatt taaaaatatg 807
 Phe Ser Pro Ala
 175
 atagtgtata aatgaaaaa aaaaaaaaa 836

<210> 66
 <211> 197
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..22

<400> 66
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 Leu Ala Ile Leu Ala Ile Leu Leu Thr Arg Trp Ala Arg Arg Lys Gln
 -5 1 5 10
 Ser Glu Met Tyr Ile Ser Arg Tyr Ser Ser Glu Gln Ser Ala Arg Leu
 15 20 25
 Leu Asp Tyr Glu Asp Gly Arg Gly Ser Arg His Ala Tyr Ser Thr Gln
 30 35 40
 Ser Glu Arg Ser Lys Arg Asp Tyr Thr Pro Ser Thr Asn Ser Leu Ala
 45 50 55
 Leu Ser Arg Ser Ser Ile Ala Leu Pro Gln Gly Ser Met Ser Ser Ile
 60 65 70
 Lys Cys Leu Gln Thr Thr Glu Glu Pro Pro Ser Arg Thr Ala Gly Ala
 75 80 85 90
 Met Met Gln Phe Thr Ala Pro Ile Pro Gly Ala Thr Gly Pro Ile Lys
 95 100 105
 Leu Ser Gln Lys Thr Ile Val Gln Thr Leu Gly Pro Ile Val Gln Tyr
 110 115 120
 Pro Gly Ser Asn Gly Arg Ile Asn Ile Ser Gln Leu Thr Ser Glu Asp
 125 130 135
 Leu Thr Gly Ala Lys Gly Arg Val Thr Ser Gly Pro Gln Phe Pro Asn
 140 145 150
 Ser His His Val Pro Glu Asn Leu His Gly Tyr Met Asn Ser Leu Ser
 155 160 165 170
 Leu Phe Ser Pro Ala
 175

<210> 67
 <211> 789
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..62

<220>
 <221> CDS
 <222> 63..572

<220>
 <221> 3'UTR
 <222> 573..789

<220>
 <221> polyA_signal
 <222> 750..755

<220>
 <221> polyA_site
 <222> 774..789

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<400> 67
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ga atg cgg ctt caa ggg gct atc ttt gtg ctc ctg ccc cac ctg ggg 107
Met Arg Leu Gln Gly Ala Ile Phe Val Leu Leu Pro His Leu Gly
1 5 10 15
ccc atc ctg gtc tgg ctg ttc act cgt gat cac atg tct ggt tgg tgt 155
Pro Ile Leu Val Trp Leu Phe Thr Arg Asp His Met Ser Gly Trp Cys
20 25 30
gag ggc cgg agg atg ctg tcc tgg tgc cca ttc tac aaa gtc tta ttg 203
Glu Gly Pro Arg Met Leu Ser Trp Cys Pro Phe Tyr Lys Val Leu Leu
35 40 45
ctt gta cag aca gcc atc tac tct gtc gtg ggc tat gcc tcc tac ctg 251
Leu Val Gln Thr Ala Ile Tyr Ser Val Val Gly Tyr Ala Ser Tyr Leu
50 55 60
gtg tgg aag gac ctg gga ggg ggc ttg ggg tgg ccc ctg gcc ctg cct 299
Val Trp Lys Asp Leu Gly Gly Gly Leu Gly Trp Pro Leu Ala Leu Pro
65 70 75
ctt cgc ctc tat gct gtt cag ctc acc atc agc tgg act gtc ctg gtt 347
Leu Arg Leu Tyr Ala Val Gln Leu Thr Ile Ser Trp Thr Val Leu Val
80 85 90 95
ctc ttt ttc aca gtc cac aac cct ggt ctg gcc ctg ctg cac ctg ctg 395
Leu Phe Phe Thr Val His Asn Pro Gly Leu Ala Leu Leu His Leu Leu
100 105 110
ctg ctg tat ggg ctg gtg gtg agc aca gca ctg atc tgg cat ccc atc 443
Leu Leu Tyr Gly Leu Val Val Ser Thr Ala Leu Ile Trp His Pro Ile
115 120 125
aac aaa ctg gct gcc ctg tta ctg ctg ccc tac cta gcc tgg ctc acc 491
Asn Lys Leu Ala Ala Leu Leu Leu Leu Pro Tyr Leu Ala Trp Leu Thr
130 135 140
gtg act tca gcc ctc acc tac cac ctg tgg agg gac agc ctt tgt cca 539
Val Thr Ser Ala Leu Thr Tyr His Leu Trp Arg Asp Ser Leu Cys Pro
145 150 155
gtg cac cag cct cag ccc acg gag aag agt gac tgaggcccta gggcatggga 592
Val His Gln Pro Gln Pro Thr Glu Lys Ser Asp
160 165 170
gaggagggac gccagggtg gggaggaaga gtctgcaagc agggctgtgg agttagggtt 652
caccccaatg ggaccaccct cctgggtccc ctgggtccgt ttttccttag aaatcagaga 712
aatgggaaag ggggggaaac tgattttaca cttaaataat aaaatcctat tagtaactcc 772
gaaaaaaaaa aaaaaaaa 789

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<210> 68
 <211> 170
 <212> PRT
 <213> Homo sapiens

<400> 68

Met Arg Leu Gln Gly Ala Ile Phe Val Leu Leu Pro His Leu Gly Pro
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 Ile Leu Val Trp Trp Leu Phe Thr Arg Asp His Met Ser Gly Trp Cys Glu
 20 25 30
 Gly Pro Arg Met Leu Ser Trp Cys Pro Phe Tyr Lys Val Leu Leu Leu
 35 40 45
 Val Gln Thr Ala Ile Tyr Ser Val Val Gly Tyr Ala Ser Tyr Leu Val
 50 55 60
 Trp Lys Asp Leu Gly Gly Gly Leu Gly Trp Pro Leu Ala Leu Pro Leu
 65 70 75 80
 Arg Leu Tyr Ala Val Gln Leu Thr Ile Ser Trp Thr Val Leu Val Leu
 85 90 95
 Phe Phe Thr Val His Asn Pro Gly Leu Ala Leu Leu His Leu Leu Leu
 100 105 110
 Leu Tyr Gly Leu Val Val Ser Thr Ala Leu Ile Trp His Pro Ile Asn
 115 120 125
 Lys Leu Ala Ala Leu Leu Leu Leu Pro Tyr Leu Ala Trp Leu Thr Val
 130 135 140
 Thr Ser Ala Leu Thr Tyr His Leu Trp Arg Asp Ser Leu Cys Pro Val
 145 150 155 160
 His Gln Pro Gln Pro Thr Glu Lys Ser Asp
 165 170

<210> 69
 <211> 2556
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..66
 <220>
 <221> CDS
 <222> 67..2427

<220>
 <221> 3'UTR
 <222> 2428..2556

<220>
 <221> polyA_signal
 <222> 2522..2527

<220>
 <221> polyA_site
 <222> 2541..2556

<400> 69
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 cgcacc atg ttc cgc ctc tgg ttg ctg ctg gcc ggg ctc tgc gcc ctc 108
 Met Phe Arg Leu Trp Leu Leu Ala Gly Leu Cys Gly Leu
 -15 -10 -5
 ctg gcg tca aga ccc ggt ttt caa aat tca ctt cta cag atc gta att 156
 Leu Ala Ser Arg Pro Gly Phe Gln Asn Ser Leu Leu Gln Ile Val Ile
 1 5 10 15
 cca gag aaa atc caa aca aat aca aat gac agt tca gaa ata gaa tat 204
 Pro Glu Lys Ile Gln Thr Asn Thr Asn Asp Ser Ser Glu Ile Glu Tyr
 20 25 30
 gaa caa ata tcc tat att att cca ata gat gag aaa ctg tac act gtg 252
 Glu Gln Ile Ser Tyr Ile Ile Pro Ile Asp Glu Lys Leu Tyr Thr Val
 35 40 45
 cac ctt aaa caa aga tat ttt tta aca gat aat ttt atg atc tat ttg 300

His	Leu	Lys	Gln	Arg	Tyr	Phe	Leu	Thr	Asp	Asn	Phe	Met	Ile	Tyr	Leu	
	50						55					60				
tac	aat	caa	gga	tct	atg	aat	act	tat	tct	tca	gat	att	cag	act	caa	348
Tyr	Asn	Gln	Gly	Ser	Met	Asn	Thr	Tyr	Ser	Ser	Asp	Ile	Gln	Thr	Gln	
	65					70					75					
tgc	tac	tat	caa	gga	aat	att	gaa	gaa	tat	cca	gat	tcc	atg	gtc	aca	396
Cys	Tyr	Tyr	Gln	Gly	Asn	Ile	Glu	Glu	Tyr	Pro	Asp	Ser	Met	Val	Thr	
	80				85					90				95		
ctc	agc	acg	tgc	tct	gga	cta	aga	gga	ata	ctg	caa	ttt	gaa	aat	gtt	444
Leu	Ser	Thr	Cys	Ser	Gly	Leu	Arg	Gly	Ile	Leu	Gln	Phe	Glu	Asn	Val	
				100					105					110		
tct	tat	gga	att	gag	cct	ctg	gaa	tct	gca	gtt	gaa	ttt	cag	cat	gtt	492
Ser	Tyr	Gly	Ile	Glu	Pro	Leu	Glu	Ser	Ala	Val	Glu	Phe	Gln	His	Val	
			115						120				125			
ctt	cac	aaa	tta	aag	aat	gaa	gac	aat	gat	att	gca	att	ttt	att	gac	540
Leu	His	Lys	Leu	Lys	Asn	Glu	Asp	Asn	Asp	Ile	Ala	Ile	Phe	Ile	Asp	
		130				135					140					
aga	agc	ctg	aaa	gaa	caa	cca	atg	gat	gac	aac	att	ttt	ata	agt	gaa	588
Arg	Ser	Leu	Lys	Glu	Gln	Pro	Met	Asp	Asp	Asn	Ile	Phe	Ile	Ser	Glu	
		145				150					155					
aaa	tca	gaa	cca	gct	gtt	cca	gat	tta	ttt	cct	ctt	tat	cta	gaa	atg	636
Lys	Ser	Glu	Pro	Ala	Val	Pro	Asp	Leu	Phe	Pro	Leu	Tyr	Leu	Asu	Met	
		160				165				170				175		
cat	att	gtg	gtg	gac	aaa	act	ttg	tat	gat	tac	tggt	ggc	tct	gat	agc	684
His	Ile	Val	Val	Asp	Lys	Thr	Leu	Tyr	Asp	Tyr	Trp	Gly	Ser	Asp	Ser	
				180					185					190		
atg	ata	gta	aca	aat	aaa	gtc	atc	gaa	att	gtt	ggc	ctt	gca	aat	tca	732
Met	Ile	Val	Thr	Asn	Lys	Val	Ile	Glu	Ile	Val	Gly	Leu	Ala	Asn	Ser	
			195					200					205			
atg	ttc	acc	caa	ttt	aaa	gtt	act	att	gtg	ctg	tca	tca	ttg	gag	tta	780
Met	Phe	Thr	Gln	Phe	Lys	Val	Thr	Ile	Val	Leu	Ser	Ser	Leu	Glu	Leu	
		210				215					220					
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Trp	Ser	Asp	Glu	Asn	Lys	Ile	Ser	Thr	Val	Gly	Glu	Ala	Asp	Glu	Leu	
		225				230					235					
ttg	caa	aaa	ttt	tta	gaa	tggt	aaa	caa	tct	tat	ctt	aac	cta	agg	cct	876
Leu	Gln	Lys	Phe	Leu	Glu	Trp	Lys	Gln	Ser	Tyr	Leu	Asn	Leu	Arg	Pro	
		240				245				250				255		
cat	gat	att	gca	tat	cta	cta	att	tat	atg	gat	tat	cct	cgt	tat	ttg	924
His	Asp	Ile	Ala	Tyr	Leu	Leu	Ile	Tyr	Met	Asp	Tyr	Pro	Arg	Tyr	Leu	
			260						265					270		
gga	gca	gtg	ttt	cct	gga	aca	atg	tgt	att	act	cgt	tat	tct	gca	gga	972
Gly	Ala	Val	Phe	Pro	Gly	Thr	Met	Cys	Ile	Thr	Arg	Tyr	Ser	Ala	Gly	
			275						280					285		
gtc	gca	ttg	tac	ccc	aag	gag	ata	act	ctg	gag	gca	ttt	gca	gtt	att	1020
Val	Ala	Leu	Tyr	Pro	Lys	Glu	Ile	Thr	Leu	Glu	Ala	Phe	Ala	Val	Ile	
		290						295					300			
gtc	acc	cag	atg	ctg	gca	ctc	agt	ctg	gga	ata	tca	tat	gac	gac	cca	1068
Val	Thr	Gln	Met	Leu	Ala	Leu	Ser	Leu	Gly	Ile	Ser	Tyr	Asp	Asp	Pro	
		305				310					315					
aag	aaa	tgt	caa	tgt	tca	gaa	tcc	acc	tgt	ata	atg	aat	cca	gaa	gtt	1116
Lys	Lys	Cys	Gln	Cys	Ser	Glu	Ser	Thr	Cys	Ile	Met	Asn	Pro	Glu	Val	
		320				325				330				335		
gtg	caa	tcc	aat	ggt	gtg	aag	act	ttt	agc	agt	tgc	agt	ttg	agg	agc	1164
Val	Gln	Ser	Asn	Gly	Val	Lys	Thr	Phe	Ser	Ser	Cys	Ser	Leu	Arg	Ser	
			340						345					350		
ttt	caa	aat	ttc	att	tca	aat	gtg	ggt	gtc	aaa	tgt	ctt	cag	aat	aag	1212
Phe	Gln	Asn	Phe	Ile	Ser	Asn	Val	Gly	Val	Lys	Cys	Leu	Gln	Asn	Lys	
			355						360					365		
cca	caa	atg	caa	aaa	aaa	tct	ccg	aaa	cca	gtc	tgt	ggc	aat	ggc	aga	1260
Pro	Gln	Met	Gln	Lys	Lys	Ser	Pro	Lys	Pro	Val	Cys	Gly	Asn	Gly	Arg	
			370					375					380			
ttg	gag	gga	aat	gaa	atc	tgt	gat	tgt	ggg	act	gag	gct	caa	tgt	gga	1308

Leu	Glu	Gly	Asn	Glu	Ile	Cys	Asp	Cys	Gly	Thr	Glu	Ala	Gln	Cys	Gly	
cct	385	agc	tgt	tgt	gat	ttt	cga	act	tgt	gta	cctg	aaa	gac	gga	gca	1356
Pro	Ala	Ser	Cys	Cys	Asp	Phe	Arg	Thr	Cys	Val	Leu	Lys	Asp	Gly	Ala	
400					405					410					415	
aaa	tgt	tat	aaa	gga	ctg	tgc	Cys	aaa	gac	tgt	caa	att	tta	caa	tca	1404
Lys	Cys	Thr	Lys	Gly	Leu	Cys	Lys	Lys	Asp	Cys	Gln	Ile	Gln	Gln	Ser	
				420					425					430		
ggc	ggt	gaa	tgt	agg	ccg	aaa	gca	cct	gaa	tgt	gac	atc	gct	gaa		1452
Gly	Val	Glu	Cys	Arg	Pro	Lys	Ala	His	Pro	Glu	Cys	Asp	Ile	Ala	Glu	
				435				440					445			
aat	tgt	aat	gga	agc	tca	cca	gaa	tgt	ggg	cct	gac	ata	cct	tta	atc	1500
Asn	Cys	Asn	Gly	Ser	Ser	Pro	Glu	Cys	Gly	Pro	Asp	Ile	Thr	Leu	Ile	
				450				455				460				
aat	gga	ctt	tca	tgc	aaa	aat	aat	aag	ttt	att	tgt	tat	gac	gga	gac	1548
Asn	Gly	Leu	Ser	Cys	Lys	Asn	Asn	Lys	Phe	Ile	Cys	Tyr	Asp	Gly	Asp	
				465			470			475						
tgc	cat	gat	ctc	gat	gca	cgt	tgt	gag	agt	gta	ttt	gga	aaa	ggg	tca	1596
Cys	His	Asp	Leu	Asp	Ala	Arg	Cys	Glu	Ser	Val	Phe	Gly	Lys	Gly	Ser	
480					485					490				495		
aga	aat	gct	cca	ttt	gcc	tgc	tat	gaa	gaa	ata	caa	tct	caa	tca	gac	1644
Arg	Asn	Ala	Pro	Phe	Ala	Cys	Tyr	Glu	Glu	Ile	Gln	Ser	Gln	Ser	Asp	
				500				505						510		
aga	ttt	ggg	aac	tgt	ggg	agg	gat	aga	aat	aac	aaa	tat	gtg	ttc	tgt	1692
Arg	Phe	Gly	Asn	Cys	Gly	Arg	Asp	Arg	Asn	Lys	Tyr	Val	Phe	Cys		
				515			520				525					
gga	tgg	agg	aat	ctt	ata	tgt	gga	aga	tta	ggt	tgt	acc	tac	cct	act	1740
Gly	Trp	Arg	Asn	Leu	Ile	Cys	Gly	Arg	Leu	Val	Cys	Thr	Tyr	Pro	Thr	
				530			535				540					
cga	aag	cct	ttc	cat	caa	gaa	aat	ggg	gat	gtg	att	tat	gct	ttc	gta	1788
Arg	Lys	Pro	Phe	His	Gln	Glu	Asn	Gly	Asp	Val	Ile	Tyr	Ala	Phe	Val	
				545			550				555					
cga	gat	tct	gta	tgc	ata	acc	gta	gac	tac	aaa	ttg	cct	cga	aca	ggt	1836
Arg	Asp	Ser	Val	Cys	Ile	Thr	Val	Asp	Tyr	Lys	Leu	Pro	Arg	Thr	Val	
560					565					570				575		
cca	gat	cca	ctg	gct	gtc	aaa	aat	ggc	tct	cag	tgt	gat	att	ggg	agg	1884
Pro	Asp	Pro	Leu	Ala	Val	Lys	Asn	Gly	Ser	Gln	Cys	Asp	Ile	Gly	Arg	
				580					585					590		
ggt	tgt	gta	aat	cgt	gaa	tgt	gta	gaa	tca	agg	ata	att	aag	gct	tca	1932
Val	Cys	Val	Asn	Arg	Glu	Cys	Val	Glu	Ser	Arg	Ile	Ile	Lys	Ala	Ser	
				595				600					605			
gca	cat	ggt	tgt	tca	caa	gat	tgt	tct	gga	cat	gga	gtg	tgt	gat	tcc	1980
Ala	His	Val	Cys	Ser	Gln	Gln	Cys	Ser	Gly	His	Gly	Val	Gly	Asp	Ser	
				610			615				620					
aga	aac	agc	tgc	cat	tgt	tgc	cca	ggc	tat	aag	cct	cca	aac	tgc	caa	2028
Arg	Asn	Lys	Cys	His	Cys	Ser	Pro	Gly	Tyr	Lys	Pro	Pro	Asn	Cys	Gln	
				625			630				635					
ata	cgt	tcc	aaa	gga	ttt	tcc	ata	ttt	cct	gag	gaa	gat	atg	ggg	tca	2076
Ile	Arg	Ser	Lys	Gly	Phe	Ser	Ile	Phe	Pro	Glu	Glu	Asp	Met	Gly	Ser	
640					645					650				655		
atc	atg	gaa	aga	gca	tct	ggg	aag	act	gaa	aac	acc	tgg	cct	cta	ggt	2124
Ile	Met	Glu	Arg	Ala	Ser	Gly	Lys	Thr	Gly	Ala	Asn	Thr	Leu	Leu	Gly	
				660				665					670			
ttc	ctc	att	gct	ctt	cct	att	ctc	att	gta	aca	acc	gca	ata	ggt	ttg	2172
Phe	Leu	Ile	Ala	Leu	Pro	Ile	Leu	Ile	Val	Thr	Thr	Ala	Ile	Val	Leu	
				675				680					685			
gca	agg	aaa	cag	ttg	aaa	aac	tgg	ttc	gcc	aag	gaa	gag	gaa	ttc	cca	2220
Ala	Arg	Lys	Gln	Leu	Lys	Asn	Trp	Phe	Ala	Lys	Glu	Glu	Glu	Phe	Pro	
				690			695				700					
agt	agc	gaa	tct	aaa	tgc	gaa	ggg	agc	aca	cag	aca	tat	gcc	agc	caa	2268
Ser	Ser	Glu	Ser	Lys	Ser	Glu	Gly	Ser	Thr	Gln	Thr	Tyr	Ala	Ser	Gln	
				705			710				715					
tcc	agc	tca	aaa	qgc	agc	act	cag	aca	tat	gcc	ggc	caa	acc	aga	tca	2316

Ser Ser Ser Glu Gly Ser Thr Gln Thr Tyr Ala Gly Gln Thr Arg Ser
 720 725 730 735
 gaa agc agc agt caa gct gat act agc aaa tcc aaa tca gaa gat agt 2364
 Glu Ser Ser Ser Gln Ala Asp Thr Ser Lys Ser Lys Ser Glu Asp Ser
 740 745 750
 gct gaa gca tat act agc aga tcc aaa tca cag gac agt acc caa aca 2412
 Ala Glu Ala Tyr Thr Ser Arg Ser Lys Ser Gln Asp Ser Thr Gln Thr
 755 760 765
 caa agc agt agt aac tagtgattcc ttcagaaggc aacggataac atcgagagtc 2467
 Gln Ser Ser Ser Asn
 770
 tcgctaagaa atgaaaattc tgtctttcct tccgtggtca cagctgaaag aaacaataaa 2527
 ttgagtgtgg accaaaaaaa aaaaaaaa 2556

<210> 70

<211> 787

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> 1..16

<400> 70

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 Ser Arg Pro Gly Phe Gln Asn Ser Leu Leu Gln Ile Val Ile Pro Glu
 1 5 10 15
 Lys Ile Gln Thr Asn Thr Asn Asp Ser Ser Glu Ile Glu Tyr Glu Gln
 20 25 30
 Ile Ser Tyr Ile Ile Pro Ile Asp Glu Lys Leu Tyr Thr Val His Leu
 35 40 45
 Lys Gln Arg Tyr Phe Leu Thr Asp Asn Phe Met Ile Tyr Leu Tyr Asn
 50 55 60
 Gln Gly Ser Met Asn Thr Tyr Ser Ser Asp Ile Gln Thr Gln Cys Tyr
 65 70 75 80
 Tyr Gln Gly Asn Ile Glu Glu Tyr Pro Asp Ser Met Val Thr Leu Ser
 85 90 95
 Thr Cys Ser Gly Leu Arg Gly Ile Leu Gln Phe Glu Asn Val Ser Tyr
 100 105 110
 Gly Ile Glu Pro Leu Glu Ser Ala Val Glu Phe Gln His Val Leu His
 115 120 125
 Lys Leu Lys Asn Glu Asp Asn Asp Ile Ala Ile Phe Ile Asp Arg Ser
 130 135 140
 Leu Lys Glu Gln Pro Met Asp Asp Asn Ile Phe Ile Ser Glu Lys Ser
 145 150 155 160
 Glu Pro Ala Val Pro Asp Leu Phe Pro Leu Tyr Leu Glu Met His Ile
 165 170 175
 Val Val Asp Lys Thr Leu Tyr Asp Tyr Trp Gly Ser Asp Ser Met Ile
 180 185 190
 Val Thr Asn Lys Val Ile Glu Ile Val Gly Leu Ala Asn Ser Met Phe
 195 200 205
 Thr Gln Phe Lys Val Thr Ile Val Leu Ser Ser Leu Glu Leu Trp Ser
 210 215 220
 Asp Glu Asn Lys Ile Ser Thr Val Gly Glu Ala Asp Glu Leu Leu Gln
 225 230 235 240
 Lys Phe Leu Glu Trp Lys Gln Ser Tyr Leu Asn Leu Arg Pro His Asp
 245 250 255
 Ile Ala Tyr Leu Leu Ile Tyr Met Asp Tyr Pro Arg Tyr Leu Gly Ala
 260 265 270
 Val Phe Pro Gly Thr Met Cys Ile Thr Arg Tyr Ser Ala Gly Val Ala
 275 280 285
 Leu Tyr Pro Lys Glu Ile Thr Leu Glu Ala Phe Ala Val Ile Val Thr

<211> 1603
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 1..7

<220>
 <221> CDS
 <222> 8..763

<220>
 <221> 3'UTR
 <222> 764..1603

<220>
 <221> polyA_signal
 <222> 1562..1567

<220>
 <221> polyA_site
 <222> 1588..1603

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 Met Gly Pro His Leu His Leu Cys Leu Cys Val Pro Asp Leu
 -15 -10 -5
 cgg tca ctc cgt gtc tgt gtg tcc ctg tgg tct gtc cac cac agg cca 97
 Arg Ser Leu Arg Val Cys Val Ser Leu Trp Ser Val His His Arg Pro
 1 5 10
 cac gag tcc ctg gcc cgg gag gag gcc ctg act gca ctt ggg aag ctg 145
 His Glu Ser Leu Ala Arg Glu Glu Ala Leu Thr Ala Leu Gly Lys Leu
 15 20 25 30
 ctg tac ctg tta gat ggg atg ctg gat ggg cag gtg aac agt ggt ata 193
 Leu Tyr Leu Leu Asp Gly Met Leu Asp Gly Gln Val Asn Ser Gly Ile
 35 40 45
 gca gcc act cca gcc tct gct gca gca gcc acc ctg gat gtg gct gtt 241
 Ala Ala Thr Pro Ala Ser Ala Ala Ala Thr Leu Asp Val Ala Val
 50 55 60
 cgg aga ggc ctg tcc cac gca gcc cag agg ctg ctg tgc gtg gcc ctg 289
 Arg Arg Gly Leu Ser His Ala Ala Gln Arg Leu Leu Cys Val Ala Leu
 65 70 75
 gga cag ctg gac cgg cct cca gac ctg gcc cat gac ggg agg agt ctg 337
 Gly Gln Leu Asp Arg Pro Pro Asp Leu Ala His Asp Gly Arg Ser Leu
 80 85 90
 tgg ctg aac atc agg ggc aag gag gcg gct gcc cta tcc atg ttc cat 385
 Trp Leu Asn Ile Arg Gly Lys Glu Ala Ala Ala Leu Ser Met Phe His
 95 100 105 110
 gtc tcc acg cca ctg cca gtg atg acc ggt ggt ttc ctg agc tgc atc 433
 Val Ser Thr Pro Leu Pro Val Met Thr Gly Gly Phe Leu Ser Cys Ile
 115 120 125
 ttg ggc ttg gtg ctg ccc ctg gcc tat ggc ttc cag cct gac ctg gtg 481
 Leu Gly Leu Val Leu Pro Leu Ala Tyr Gly Phe Gln Pro Asp Leu Val
 130 135 140
 ctg gtg gcg ctg ggg cct ggc cat ggc ctg cag ggc ccc cac gst gca 529
 Leu Val Ala Leu Gly Pro Gly His Gly Leu Gln Gly Pro His Xaa Ala
 145 150 155
 ctc ctg gct gca atg ctt cgg ggg ctg gca ggg ggc cga gtc ctg gcc 577
 Leu Leu Ala Ala Met Leu Arg Gly Leu Ala Gly Gly Arg Val Leu Ala
 160 165 170
 ctc ctg gag gag aac tcc aca ccc cag cta gca ggg atc ctg gcc cgg 625
 Leu Leu Glu Glu Asn Ser Thr Pro Gln Leu Ala Gly Ile Leu Ala Arg

175	180	185	190	
gtg ctg aat gga gag gca cct cct agc cta ggc cct tcc tct gtg gcc				673
Val Leu Asn Gly Glu Ala Pro Pro Ser Leu Gly Pro Ser Ser Val Ala				
	195	200	205	
tcc cca gag gac gtc cag gcc ctg atg tac ctg aga ggg cag ctg gag				721
Ser Pro Glu Asp Val Gln Ala Leu Met Tyr Leu Arg Gly Gln Leu Glu				
	210	215	220	
cct cag tgg aag atg ttg cag tgc cat cct cac ctg gtg gct				763
Pro Gln Trp Lys Met Leu Gln Cys His Pro His Leu Val Ala				
	225	230	235	
tgaatatcggc caaggtgggga gcatttacac cgcagaaatg acacgcgacg ccagcgcccc				823
ggcgccgcgga tccgggacccc aagccccacgg ctccctcgac tctggggcac ggaacccccg				883
ccaactccaa tccccgcgcg ccgccctctc ccaccccgctg ttcccccgct ccacccctca				943
cctcaactcg cccccgcccc acccatcgcg ccccgcgcggc tgttattgtt cggctgggct				1003
cggtcgggcg ctgtctccct cggtctcgcg ggtgtcagtt cgtccggcct cctcacagcc				1063
cctcaactccc ggcggtgtgac agcagcagcg gcggcgggcg gcggcgccctg gcgtttcgag				1123
gctgagcggc accgggggtg ggccgcggag gaggagcagc agcgggagga ggagccgtgt				1183
gccttggcac tgagcggcg cgcccatggc gtacgcctat ctcttcaagt acatcataat				1243
cgggcgacaca ggtgttggtta aatcatgctt attgtctacag ttacagaca agaggttcag				1303
ccagtgcagt acctactat tgggttagag ttcggtgctc gaatgataac tattgatggg				1363
aaacagataa aacttcagat atgggatacg gcagggcaag aatcctttcg ttccatcaca				1423
aggtcgattt acagaggtgc agcaggagct ttactagttt acgatattac acggagagat				1483
acattcaacc acttgacaac ctggttagaa gatgcccgcc agcattccaa ttcccaacatg				1543
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<210> 72
 <211> 252
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..17

<220>
 <221> UNSURE
 <222> 173
 <223> Xaa = Ala, Gly

<400> 72
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 1 5 10 15
 Ser Leu Ala Arg Glu Glu Ala Leu Thr Ala Leu Gly Lys Leu Leu Tyr
 20 25 30
 Leu Leu Asp Gly Met Leu Asp Gly Gln Val Asn Ser Gly Ile Ala Ala
 35 40 45
 Thr Pro Ala Ser Ala Ala Ala Thr Leu Asp Val Ala Val Arg Arg
 50 55 60
 Gly Leu Ser His Ala Ala Gln Arg Leu Leu Cys Val Ala Leu Gly Gln
 65 70 75
 Leu Asp Arg Pro Pro Asp Leu Ala His Asp Gly Arg Ser Leu Trp Leu
 80 85 90 95
 Asn Ile Arg Gly Lys Glu Ala Ala Ala Leu Ser Met Phe His Val Ser
 100 105 110
 Thr Pro Leu Pro Val Met Thr Gly Gly Phe Leu Ser Cys Ile Leu Gly
 115 120 125
 Leu Val Leu Pro Leu Ala Tyr Gly Phe Gln Pro Asp Leu Val Leu Val
 130 135 140
 Ala Leu Gly Pro Gly His Gly Leu Gln Gly Pro His Xaa Ala Leu Leu
 145 150 155
 Ala Ala Met Leu Arg Gly Leu Ala Gly Gly Arg Val Leu Ala Leu Leu

160	165	170	175
Glu Glu Asn Ser Thr	Pro Gln Leu Ala Gly Ile Leu Ala Arg Val Leu		
	180	185	190
Asn Gly Glu Ala Pro Pro Ser Leu Gly Pro Ser Ser Val Ala Ser Pro			
	195	200	205
Glu Asp Val Gln Ala Leu Met Tyr Leu Arg Gly Gln Leu Glu Pro Gln			
	210	215	220
Trp Lys Met Leu Gln Cys His Pro His Leu Val Ala			
	225	230	235

<210> 73
 <211> 879
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..8

<220>
 <221> CDS
 <222> 9..395

<220>
 <221> 3'UTR
 <222> 396..879

<220>
 <221> polyA_site
 <222> 864..879

<400> 73
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 Met Ala Val Leu Leu Leu Leu Arg Ala Leu Arg Arg Gly
 -15 -10 -5
 cca gcc cgg ggt cct cgg cgg ctg tgg gcc cca gcc cgg gcc tgg agt 98
 Pro Gly Pro Gly Pro Arg Pro Leu Trp Gly Pro Gly Pro Ala Trp Ser
 1 5 10 15
 cca ggg ttc ccc gcc agg ccc ggg agg ggg cgg ccg tac atg gcc agc 146
 Pro Gly Phe Pro Ala Arg Pro Gly Arg Gly Arg Pro Tyr Met Ala Ser
 20 25 30
 agg cct cgg ggg gac ctc gcc gag gct gga gcc cga gct ctg cag agc 194
 Arg Pro Pro Gly Asp Leu Ala Glu Ala Gly Gly Arg Ala Leu Gln Ser
 35 40 45
 tta caa ttg aga ctg cta acc cct acc ttt gaa ggg atc aac gga ttg 242
 Leu Gln Leu Arg Leu Leu Thr Pro Thr Phe Glu Gly Ile Asn Gly Leu
 50 55 60
 ttg ttg aaa caa cat tta gtt cag aat cca gtc aga ctc tgg caa ctt 290
 Leu Lys Lys Gln His Leu Val Gln Asn Pro Val Arg Leu Trp Gln Leu
 65 70 75
 tta ggt ggt act ttc tat ttt aac acc tca agg ttg aag cag aag aat 338
 Leu Gly Gly Thr Phe Tyr Phe Asn Thr Ser Arg Leu Lys Gln Lys Asn
 80 85 90 95
 aag gag aag gat aag tcg aag ggg aag gcg cct gaa gag gac gaa ggt 386
 Lys Glu Lys Asp Lys Ser Lys Gly Lys Ala Pro Glu Glu Asp Glu Gly
 100 105 110
 ata ttc atc tgatgttctt cagtcagtag ctgcctctgg atgtctttac 435
 Ile Phe Ile
 rtttctgttt wcttttttagc aaggtgaaac cagtcctggam aatgggggaga tggggccgggt 495
 gcagtggtct acacttgtaa tcgaaacgct ttggggaggcc caggtggaag gatcacttga 555
 ggcctataacc acatagctag accctgtctc actgcaaatt aaaaggctgg gcgtggtggc 615
 tcacacctgt aatcccagca ctttgggagg ctgaggcagg cggatcact gcacctggc 675
 caacatgggtg aaaccccgct tttactaaaa atagaaaatt agccgggcgt gatggcacac 735

gcctgtaatc ccagctactc gggaggctga ggcaggagaa ttgcttgaac ctggggagggtg 795
 gaggttgctg tgagtggaga tcatgccatt gcactccagc ctgagcaaca agagcaaaac 855
 tccatcccaa aaaaaaaaaa aaaa 879

<210> 74
 <211> 129
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..16

<400> 74
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 -15 -10 -5
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 1 5 10 15
 Phe Pro Ala Arg Pro Gly Arg Gly Arg Pro Tyr Met Ala Ser Arg Pro
 20 25 30
 Pro Gly Asp Leu Ala Glu Ala Gly Gly Arg Ala Leu Gln Ser Leu Gln
 35 40 45
 Leu Arg Leu Leu Thr Pro Thr Phe Glu Gly Ile Asn Gly Leu Leu Leu
 50 55 60
 Lys Gln His Leu Val Gln Asn Pro Val Arg Leu Trp Gln Leu Leu Gly
 65 70 75
 Gly Thr Phe Tyr Phe Asn Thr Ser Arg Leu Lys Gln Lys Asn Lys Glu
 85 90 95
 Lys Asp Lys Ser Lys Gly Lys Ala Pro Glu Glu Gly Ile Phe
 100 105 110
 Ile

<210> 75
 <211> 1634
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..87

<220>
 <221> CDS
 <222> 88..1269

<220>
 <221> 3'UTR
 <222> 1270..1634

<220>
 <221> polyA_signal
 <222> 1594..1599

<220>
 <221> polyA_site
 <222> 1619..1634

<400> 75
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 agagtcatcg cctgtcgggg ctaggat atg atg ggt gtg ttt gta gtt gct gct 114
 Met Met Gly Val Phe Val Val Ala Ala
 1 5
 aag cga acg ccc ttt gga gct tac gga ggc ctt ctg aaa gac ttc act 162

Lys	Arg	Thr	Pro	Phe	Gly	Ala	Tyr	Gly	Gly	Leu	Leu	Lys	Asp	Phe	Thr		
10				15					20					25			
gct	act	gac	ttg	tct	gaa	ttt	gct	gcc	aag	gct	gcc	ttg	tct	gct	ggc	210	
Ala	Thr	Asp	Leu	30	Glu	Phe	Ala	Ala	Lys	Ala	Ala	Leu	Ser	Ala	Gly		
aaa	gtc	tca	cct	gaa	aca	ggt	gac	agt	gtg	att	atg	ggc	aat	gtc	ctg	258	
Lys	Val	Ser	Pro	Glu	Thr	Val	Asp	Ser	Val	Ile	Met	Gly	Asn	Val	Leu		
45								50				55					
cag	agt	tct	tca	gat	gct	ata	tat	ttg	gca	agg	cat	ggt	ggg	ttg	cgt	306	
Gln	Ser	Ser	Ser	Asp	Ala	Ile	Tyr	Leu	Ala	Arg	His	Val	Gly	Leu	Arg		
60							65				70						
gtg	gga	atc	cca	aag	gag	acc	cca	gct	ctc	acg	att	aat	agg	ctc	tgt	354	
Val	Gly	Ile	Pro	Lys	Glu	Thr	Pro	Ala	Leu	Thr	Ile	Asn	Arg	Leu	Cys		
75						80				85							
ggg	tct	ggg	ttt	cag	tcc	att	gtg	aat	gga	tgt	cag	gaa	att	tgt	ggt	402	
Gly	Ser	Gly	Phe	Gln	Ser	Ile	Val	Asn	Gly	Cys	Gln	Glu	Ile	Cys	Val		
90					95				100					105			
aaa	gaa	gct	gaa	ggt	ggt	tta	tgt	gga	gga	acc	gaa	agc	atg	agc	caa	450	
Lys	Glu	Ala	Glu	Val	Val	Leu	Cys	Gly	Gly	Thr	Glu	Ser	Met	Ser	Gln		
110								115						120			
gct	ccc	tac	tgt	gtc	aga	aat	gtg	cgt	ttt	gga	acc	aag	ctt	gga	tca	498	
Ala	Pro	Tyr	Cys	Val	Arg	Asn	Val	Arg	Phe	Gly	Thr	Lys	Leu	Gly	Ser		
125							130						135				
gat	atc	aag	ctg	gaa	gat	tct	tta	tgg	gta	tca	tta	aca	gat	cag	cat	546	
Asp	Ile	Lys	Leu	Glu	Asp	Ser	Leu	Trp	Val	Ser	Leu	Thr	Asp	Gln	His		
140						145						150					
gtc	cag	ctc	ccc	atg	gca	atg	act	gca	gag	aat	ctt	gct	gta	aaa	cac	594	
Val	Gln	Leu	Pro	Met	Ala	Met	Thr	Ala	Glu	Asn	Leu	Ala	Val	Lys	His		
155						160					165						
aaa	ata	agc	aga	gaa	gaa	tgt	gac	aaa	tat	gcc	ctg	cag	tca	cag	cag	642	
Lys	Ile	Ser	Ser	Arg	Glu	Glu	Cys	Asp	Lys	Tyr	Ala	Leu	Gln	Ser	Gln		
170					175					180				185			
aga	tgg	aaa	gct	gct	aat	gat	gct	ggc	tac	ttt	aat	gat	gaa	atg	gca	690	
Arg	Trp	Lys	Ala	Ala	Asn	Asp	Ala	Gly	Tyr	Phe	Asn	Asp	Glu	Met	Ala		
190								195					200				
cca	att	gaa	gtg	aag	aca	aag	aaa	gga	aaa	cag	aca	atg	cag	gta	gac	738	
Pro	Ile	Glu	Val	Lys	Thr	Lys	Lys	Gly	Lys	Gln	Thr	Met	Gln	Val	Asp		
205								210					215				
gag	cat	gct	cgg	ccc	caa	acc	acc	ctg	gaa	cag	tta	cag	aaa	ctt	cct	786	
Glu	His	Ala	Arg	Pro	Gln	Thr	Thr	Leu	Glu	Gln	Leu	Gln	Lys	Leu	Pro		
220						225						230					
cca	gta	ttc	aag	aaa	gat	gga	act	ggt	act	gca	ggg	aat	gca	tcg	ggg	834	
Pro	Val	Phe	Lys	Lys	Asp	Gly	Thr	Val	Thr	Ala	Gly	Asn	Ala	Ser	Gly		
235						240					245						
gta	gct	gat	ggg	gct	gga	gct	ggt	atc	ata	gct	agt	gaa	gat	gct	ggt	882	
Val	Ala	Asp	Gly	Ala	Gly	Ala	Val	Ile	Ile	Ala	Ser	Glu	Asp	Ala	Val		
250					255					260				265			
aag	aaa	cat	aac	ttc	aca	cca	ctg	gca	aga	att	gtg	ggc	tac	ttt	gta	930	
Lys	Lys	His	Asn	Phe	Thr	Pro	Leu	Ala	Arg	Ile	Val	Gly	Tyr	Phe	Val		
270								275						280			
tct	gga	tgt	gat	ccc	tct	atc	atg	ggg	att	ggg	cct	gtc	cct	gct	atc	978	
Ser	Gly	Cys	Asp	Pro	Ser	Ile	Met	Gly	Ile	Gly	Pro	Val	Pro	Ala	Ile		
285								290					295				
agt	ggg	gca	ctg	aag	aaa	gca	gga	ctg	agt	ctt	aag	gac	atg	gat	ttg	1026	
Ser	Gly	Ala	Leu	Lys	Lys	Ala	Gly	Leu	Ser	Leu	Lys	Asp	Met	Asp	Leu		
300						305						310					
gta	gag	gtg	aat	gaa	gct	ttt	gct	ccc	cag	tac	ttg	gct	ggt	gag	agg	1074	
Val	Glu	Val	Asn	Glu	Ala	Phe	Ala	Thr	Gln	Tyr	Leu	Ala	Val	Glu	Arg		
315						320					325						
agt	ttg	gat	ctt	gac	ata	agt	aaa	acc	aat	gtg	aat	gga	gga	gcc	att	1122	
Ser	Leu	Asp	Leu	Asp	Ile	Ser	Lys	Thr	Asn	Val	Asn	Gly	Gly	Ala	Ile		
330					335					340				345			
gct	ttg	ggg	cac	cca	ctg	gga	gga	tct	gga	tca	aga	att	act	gca	cac	1170	

Ala	Leu	Gly	His	Pro	Leu	Gly	Gly	Ser	Gly	Ser	Arg	Ile	Thr	Ala	His		
			350						355					360			
ctg	gtt	cac	gaa	tta	agg	cgt	cga	ggg	gga	aaa	tat	gcc	gtt	gga	tca	1218	
Leu	Val	His	Glu	Leu	Arg	Arg	Arg	Gly	Gly	Lys	Tyr	Ala	Val	Gly	Ser		
			365					370					375				
gct	tgc	att	gga	ggg	ggc	caa	ggg	att	gct	gtc	atc	att	cag	agc	aca	1266	
Ala	Cys	Ile	Gly	Gly	Gly	Gln	Gly	Ile	Ala	Val	Ile	Ile	Gln	Ser	Thr		
			380					385				390					
gcc	tgaagagacc	agtgagctca	ctgtgaccca	tccttactct	acttgccag											1319	
Ala																	
gccacagtaa	aacaagtgac	cttcagagca	gctgccacaa	ctggccatgc	cctgccattg	1379											
aaacagtgat	taagtttgat	caagccatgg	tgacacaaaa	atgcattgat	catgaatagg	1439											
agcccatgct	agaagtacat	tctctcagat	tgaaccagt	gaatatgat	gtattttcga	1499											
gctaaaactc	aactatagaa	gacattaaaa	gaatcgtat	tcttgccaag	taaccaccac	1559											
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aaaaaaaaaa	aaaaa					1634											

<210> 76

<211> 394

<212> PRT

<213> Homo sapiens

<400> 76

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Tyr	Gly	Gly	Leu	Leu	Lys	Asp	Phe	Thr	Ala	Thr	Asp	Leu	Ser	Glu	Phe		
			20					25					30				
Ala	Ala	Lys	Ala	Ala	Leu	Ser	Ala	Gly	Lys	Val	Ser	Pro	Glu	Thr	Val		
		35					40					45					
Asp	Ser	Val	Ile	Met	Gly	Asn	Val	Leu	Gln	Ser	Ser	Ser	Asp	Ala	Ile		
	50					55					60						
Tyr	Leu	Ala	Arg	His	Val	Gly	Leu	Arg	Val	Gly	Ile	Pro	Lys	Glu	Thr		
65					70					75				80			
Pro	Ala	Leu	Thr	Ile	Asn	Arg	Leu	Cys	Gly	Ser	Gly	Phe	Gln	Ser	Ile		
				85					90					95			
Val	Asn	Gly	Cys	Gln	Glu	Ile	Cys	Val	Lys	Glu	Ala	Glu	Val	Val	Leu		
			100						105				110				
Cys	Gly	Gly	Thr	Glu	Ser	Met	Ser	Gln	Ala	Pro	Tyr	Cys	Val	Arg	Asn		
			115				120					125					
Val	Arg	Phe	Gly	Thr	Lys	Leu	Gly	Ser	Asp	Ile	Lys	Leu	Glu	Asp	Ser		
			130				135				140						
Leu	Trp	Val	Ser	Leu	Thr	Asp	Gln	His	Val	Gln	Leu	Pro	Met	Ala	Met		
145					150					155				160			
Thr	Ala	Glu	Asn	Leu	Ala	Val	Lys	His	Lys	Ile	Ser	Arg	Glu	Glu	Cys		
			165						170					175			
Asp	Lys	Tyr	Ala	Leu	Gln	Ser	Gln	Arg	Trp	Lys	Ala	Ala	Asn	Asp			
			180					185				190					
Ala	Gly	Tyr	Phe	Asn	Asp	Glu	Met	Ala	Pro	Ile	Glu	Val	Lys	Thr	Lys		
			195				200					205					
Lys	Gly	Lys	Gln	Thr	Met	Gln	Val	Asp	Glu	His	Ala	Arg	Pro	Gln	Thr		
			210				215				220						
Thr	Leu	Glu	Gln	Leu	Gln	Lys	Leu	Pro	Pro	Val	Phe	Lys	Lys	Asp	Gly		
225					230					235				240			
Thr	Val	Thr	Ala	Gly	Asn	Ala	Ser	Gly	Val	Ala	Asp	Gly	Ala	Gly	Ala		
				245					250					255			
Val	Ile	Ile	Ala	Ser	Glu	Asp	Ala	Val	Lys	Lys	His	Asn	Phe	Thr	Pro		
			260					265				270					
Leu	Ala	Arg	Ile	Val	Gly	Tyr	Phe	Val	Ser	Gly	Cys	Asp	Pro	Ser	Ile		
			275				280					285					
Met	Gly	Ile	Gly	Pro	Val	Pro	Ala	Ile	Ser	Gly	Ala	Leu	Lys	Lys	Ala		
			290				295				300						
Gly	Leu	Ser	Leu	Lys	Asp	Met	Asp	Leu	Val	Glu	Val	Asn	Glu	Ala	Phe		
305					310					315				320			

Ala Pro Gln Tyr Leu Ala Val Glu Arg Ser Leu Asp Leu Asp Ile Ser
 325 330 335
 Lys Thr Asn Val Asn Gly Gly Ala Ile Ala Leu Gly His Pro Leu Gly
 340 345 350
 Gly Ser Gly Ser Arg Ile Thr Ala His Leu Val His Glu Leu Arg Arg
 355 360 365
 Arg Gly Gly Lys Tyr Ala Val Gly Ser Ala Cys Ile Gly Gly Gly Gln
 370 375 380
 Gly Ile Ala Val Ile Ile Gln Ser Thr Ala
 385 390

<210> 77
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 1..68

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 <221> CDS
 <222> 69..875

<220>
 <221> 3'UTR
 <222> 876..1642

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 <222> 1599..1604

<220>
 <221> polyA_site
 <222> 1627..1642

<400> 77
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 taggaatc atg gcg gct gcg ctg ttc gtg ctg ctg gga ttc gcg ctg ctg 110
 Met Ala Ala Ala Leu Phe Val Leu Leu Gly Phe Ala Leu Leu
 -20 -15 -10
 ggc acc cac gga gcc tcc ggg gct gcc ggc aca gtc ttc act acc gta 158
 Gly Thr His Gly Ala Ser Gly Ala Ala Gly Thr Val Phe Thr Thr Val
 -5 1 5 10
 gaa gac ctt ggc tcc aag ata ctc ctc acc tgc tcc ttg aat gac agc 206
 Glu Asp Leu Gly Ser Lys Ile Leu Leu Thr Cys Ser Leu Asn Asp Ser
 15 20 25
 gcc aca gag gtc aca ggg cac cgc tgg ctg aag ggg gcc gtg gtg ctg 254
 Ala Thr Glu Val Thr Gly His Arg Trp Leu Lys Gly Gly Val Val Leu
 30 35 40
 aag gag gac gcg ctg ccc ggc cag aaa acg gag ttc aag gtg gac tcc 302
 Lys Glu Asp Ala Leu Pro Gly Gln Lys Thr Glu Phe Lys Val Asp Ser
 45 50 55
 gac gac cag tgg gga gag tac tcc tgc gtc ttc ctc ccc gag ccc atg 350
 Asp Asp Gln Trp Gly Glu Tyr Ser Cys Val Phe Leu Pro Glu Pro Met
 60 65 70
 ggc acg gcc aac atc cag ctc cac ggg cct ccc aga gtg aag gcc gtg 398
 Gly Thr Ala Asn Ile Gln Leu His Gly Pro Pro Arg Val Lys Ala Val
 75 80 85 90
 aag tcg tca gaa cac atc aac gag ggg gag acg gcc atg ctg gtc tgc 446
 Lys Ser Ser Glu His Ile Asn Glu Gly Glu Thr Ala Met Leu Val Cys
 95 100 105
 aag tca gag tcc gtg cca cct gtc act gac tgg gcc tgg tac aag atc 494

Lys	Ser	Glu	Ser	Val	Pro	Pro	Val	Thr	Asp	Trp	Ala	Trp	Tyr	Lys	Ile	
			110					115					120			
act	gac	tct	gag	gac	aag	gcc	ctc	atg	aac	ggc	tcc	gag	agc	agg	ttc	542
Thr	Asp	Ser	Glu	Asp	Lys	Ala	Leu	Met	Asn	Gly	Ser	Glu	Ser	Arg	Phe	
		125					130					135				
ttc	gtg	agt	tcc	tgc	cag	ggc	ctg	tca	gag	cta	cac	att	gag	aac	ctg	590
Phe	Val	Ser	Ser	Ser	Gln	Gly	Leu	Ser	Glu	Leu	His	Ile	Glu	Asn	Leu	
		140				145					150					
aac	atg	gag	gcc	gac	ccc	ggc	cag	tac	cgg	tgc	aac	ggc	acc	agc	tcc	638
Asn	Met	Glu	Ala	Asp	Pro	Gly	Gln	Tyr	Arg	Cys	Asn	Gly	Thr	Ser	Ser	
		155				160				165					170	
aag	ggc	tcc	gac	cag	gcc	atc	atc	acg	ctc	cgc	gtg	cgc	agc	cac	ctg	686
Lys	Gly	Ser	Asp	Gln	Ala	Ile	Ile	Thr	Leu	Arg	Val	Arg	Ser	His	Leu	
			175						180					185		
gcc	gcc	ctc	tgg	ccc	ttc	ctg	ggc	atc	gtg	gct	gag	gtg	ctg	gtg	ctg	734
Ala	Ala	Leu	Trp	Pro	Phe	Leu	Gly	Ile	Val	Ala	Glu	Val	Leu	Val	Leu	
			190					195				200				
gtc	acc	atc	atc	ttc	atc	tac	gag	aag	cgc	cgg	aag	ccc	gag	gac	gtc	782
Val	Thr	Ile	Ile	Phe	Ile	Tyr	Glu	Lys	Arg	Arg	Lys	Pro	Glu	Asp	Val	
		205					210					215				
ctg	gat	gat	gac	gac	gcc	ggc	tct	gca	ccc	ctg	aag	agc	agc	ggg	cag	830
Leu	Asp	Asp	Asp	Ala	Gly	Ser	Ala	Pro	Leu	Lys	Ser	Ser	Gly	Gln		
		220			225					230						
cac	cag	aat	gac	aaa	ggc	aag	aac	gtc	cgc	cag	agg	aac	tct	tcc		875
His	Gln	Asn	Asp	Lys	Gly	Lys	Asn	Val	Arg	Gln	Arg	Asn	Ser	Ser		
		235			240					245						
tgaggcaggt	ggccccgagga	cgcctccctgc	tcgcgcgtctg	cgcgcgcgcgc	ggagtcacct	935										
cccagtgctt	gcaagattcc	aagttctcac	ctcttaaaga	aaacccaccc	cgtagattcc	995										
catcatcac	ttcctcttt	tttaaaaaag	ttgggttttc	tcatttcagg	attctgttcc	1055										
ttagagatttt	ttcctctga	agtggtttcac	gagagccccg	gagctgtctgc	ctcgcggccc	1115										
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cctcttggcc	acagaggagt	cacttgccca	caccaggggc	gaccocgtca	cagcctcaag	1415										
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aggacggccg	gctctctata	gcaccagggc	tcacgtggga	acccccctcc	caccacacgc	1595										
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<210> 78

<211> 269

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> 1..21

<400> 78

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	-5			1					5				10		
Leu	Gly	Ser	Lys	Ile	Leu	Leu	Thr	Cys	Ser	Leu	Asn	Asp	Ser	Ala	Thr
			15				20					25			
Glu	Val	Thr	Gly	His	Arg	Trp	Leu	Lys	Gly	Gly	Val	Val	Leu	Lys	Glu
	30					35					40				
Asp	Ala	Leu	Pro	Gly	Gln	Lys	Thr	Glu	Phe	Lys	Val	Asp	Ser	Asp	Asp
	45				50					55					
Gln	Trp	Gly	Glu	Tyr	Ser	Cys	Val	Phe	Leu	Pro	Glu	Pro	Met	Gly	Thr
	60				65				70				75		
Ala	Asn	Ile	Gln	Leu	His	Gly	Pro	Pro	Arg	Val	Lys	Ala	Val	Lys	Ser

	80		85		90										
Ser	Glu	His	Ile	Asn	Glu	Gly	Glu	Thr	Ala	Met	Leu	Val	Cys	Lys	Ser
	95							100					105		
Glu	Ser	Val	Pro	Pro	Val	Thr	Asp	Trp	Ala	Trp	Tyr	Lys	Ile	Thr	Asp
	110						115					120			
Ser	Glu	Asp	Lys	Ala	Leu	Met	Asn	Gly	Ser	Glu	Ser	Arg	Phe	Phe	Val
	125				130						135				
Ser	Ser	Ser	Gln	Gly	Leu	Ser	Glu	Leu	His	Ile	Glu	Asn	Leu	Asn	Met
	140				145					150				155	
Glu	Ala	Asp	Pro	Gly	Gln	Tyr	Arg	Cys	Asn	Gly	Thr	Ser	Ser	Lys	Gly
			160						165					170	
Ser	Asp	Gln	Ala	Ile	Ile	Thr	Leu	Arg	Val	Arg	Ser	His	Leu	Ala	Ala
		175					180					185			
Leu	Trp	Pro	Phe	Leu	Gly	Ile	Val	Ala	Glu	Val	Leu	Val	Leu	Val	Thr
	190						195					200			
Ile	Ile	Phe	Ile	Tyr	Glu	Lys	Arg	Arg	Lys	Pro	Glu	Asp	Val	Leu	Asp
	205				210						215				
Asp	Asp	Asp	Ala	Gly	Ser	Ala	Pro	Leu	Lys	Ser	Ser	Gly	Gln	His	Gln
	220				225					230				235	
Asn	Asp	Lys	Gly	Lys	Asn	Val	Arg	Gln	Arg	Asn	Ser	Ser			
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<210> 79

<211> 1466

<212> DNA

<213> Homo sapiens

<220>

<221> 5'UTR

<222> 1..343

<220>

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<221> 3'UTR

<222> 1145..1466

<400> 79

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gggcccaggg	agctgtcttc	tgaatccaag	ttcgtgggct	ctctcagaag	tcctcaggagc	180
ggagcagagg	tggccggcgg	gcccggtcga	ctgcgcctyt	gctttctttc	cataaccttt	240
tccttcggag	tcgaatcacg	gctgctgcga	agggtctagt	tcgggacact	agggtgcccg	300
aacgcgctga	tgccccgagt	gctcgcaggg	cttcccgcga	acc atg ctg ccg ccg		355
				Met Leu Pro Pro		
ccg cgg ccc gca gct gcc ttg gcg ctg cct gtg ctc ctg cta ctg ctg						403
Pro Arg Pro Ala Ala Ala Leu Ala Leu Pro Val Leu Leu Leu Leu Leu						
-25	-20	-15	-10			
gtg gtg ctg acg ccg ccc ccg acc ggc gca agg cca tcc cca ggc cca						451
Val Val Leu Thr Pro Pro Thr Gly Ala Arg Pro Ser Pro Gly Pro						
-5	1	5				
gat tac ctg cgg cgc ggc tgg atg cgg ctg cta gcg gag ggc gag ggc						499
Asp Tyr Leu Arg Arg Gly Trp Met Arg Leu Leu Ala Glu Gly Glu Gly						
10	15	20				
tgc gct ccc tgc cgg cca gaa gag tgc gcc gcg ccg cgg ggc tgc ctg						547
Cys Ala Pro Cys Arg Pro Glu Glu Cys Ala Ala Pro Arg Gly Cys Leu						
25	30	35				
gcg ggc agg gtg cgc gac gcg tgc ggc tgc tgc tgg gaa tgc gcc aac						595
Ala Gly Arg Val Arg Asp Ala Cys Gly Cys Cys Trp Glu Cys Ala Asn						
40	45	50	55			
ctc gag ggc cag ctc tgc gac ctg gac ccc agt gct cac ttc tac ggg						643

His Phe Tyr Gly His Cys Gly Glu Gln Leu Glu Cys Arg Leu Asp Thr
 70 75 80
 Gly Gly Asp Leu Ser Arg Gly Glu Val Pro Glu Pro Leu Cys Ala Cys
 85 90 95
 Arg Ser Gln Ser Pro Leu Cys Gly Ser Asp Gly His Thr Tyr Ser Gln
 100 105 110
 Ile Cys Arg Leu Gln Glu Ala Ala Arg Ala Arg Pro Asp Ala Asn Leu
 115 120 125 130
 Thr Val Ala His Pro Gly Pro Cys Glu Ser Gly Pro Gln Ile Val Ser
 135 140 145
 His Pro Tyr Asp Thr Trp Asn Val Thr Gly Gln Asp Val Ile Phe Gly
 150 155 160
 Cys Glu Val Phe Ala Tyr Pro Met Ala Ser Ile Glu Trp Arg Lys Asp
 165 170 175
 Gly Leu Asp Ile Gln Leu Pro Gly Asp Asp Pro His Ile Ser Val Gln
 180 185 190
 Phe Arg Gly Gly Pro Gln Arg Phe Glu Val Thr Gly Trp Leu Gln Ile
 195 200 205 210
 Gln Ala Val Arg Pro Ser Asp Glu Gly Thr Tyr Arg Cys Leu Gly Pro
 215 220 225
 Met Pro Trp Val Lys Trp Arg Pro Leu Leu Ala
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<210> 81
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 1..26

<220>
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 <222> 27..689

<220>
 <221> 3'UTR
 <222> 690..1406

<220>
 <221> polyA_signal
 <222> 1302..1307

<220>
 <221> polyA_site
 <222> 1325..1406

<400> 81
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 Gly Leu Arg Ala Leu Cys Arg Val Leu Leu Phe Leu Ser Gln Phe Cys
 -20 -15 -10
 att ctg tcg ggc ggt gaa agt act gaa atc cca cct tat gtg atg aag 149
 Ile Leu Ser Gly Gly Glu Ser Thr Glu Ile Pro Pro Tyr Val Met Lys
 -5 1 5 10
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 Cys Pro Ser Asn Gly Leu Cys Ser Arg Leu Pro Ala Asp Cys Ile Asp
 15 20 25
 tgc aca aca aat ttc tcc tgt acc tat ggg aag cct gtc act ttt gac 245
 Cys Thr Thr Asn Phe Ser Cys Thr Tyr Gly Lys Pro Val Thr Phe Asp

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<212> PRT
<213> Homo sapiens
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<221> SIGNAL
<222> 1..32
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Val	Leu	Leu	Phe	Leu	Ser	Gln	Phe	Cys	Ile	Leu	Ser	Gly	Gly	Glu	Ser
	-15					-10					-5				
Thr	Gly	Ile	Pro	Pro	Tyr	Val	Met	Lys	Cys	Pro	Ser	Asn	Gly	Leu	Cys
1				5					10					15	
Ser	Arg	Leu	Pro	Ala	Asp	Cys	Ile	Asp	Cys	Thr	Thr	Asn	Phe	Ser	Cys
		20						25					30		
Thr	Thr	Gly	Lys	Pro	Val	Thr	Phe	Asp	Cys	Ala	Val	Lys	Pro	Ser	Val

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 Arg Phe Arg Arg Trp Asn Cys Ser Ser His Ser Lys Ala Phe Gly Arg
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 atc ctg caa cag ggt cag tgt ggg gag ggg cac cct gca agg acc ctg 453
 Ile Leu Gln Gln Gly Gln Cys Gly Glu Gly His Pro Ala Arg Thr Leu
 75 80 85
 cct ccc agg ccc ctg ggg cag ccc tcc cgc cgc agg ttt cag gtc cca 501
 Pro Pro Arg Pro Leu Gly Gln Pro Ser Arg Arg Arg Phe Gln Val Pro
 90 95 100 105
 ggc ccc agc tgaccgcccc agccccgcct gattgcacct gtctgcattc 550
 Gly Pro Ser
 acagacattc gggagacggc cttcgtgttc gccatcactg cggccggcgc cagccacggc 610
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 gcgtttgtgt aactgcacaa caacgaggcg ggcaggctgg ccgtgcggag ccacacgcgc 910
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 cgtttaaag acactgtaca ggcctccctc tctagggagg tctaggtttt 1630
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 <211> 131
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..24

<400> 84
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 -5 1 5
 Leu Val Met Asp Pro Thr Ser Ile Cys Arg Lys Ala Arg Arg Leu Ala
 10 15 20
 Gly Arg Gln Ala Glu Leu Cys Gln Ala Glu Pro Glu Val Val Ala Glu
 25 30 35 40
 Leu Ala Arg Gly Ala Arg Leu Gly Val Arg Glu Cys Gln Phe Gln Phe
 45 50 55
 Arg Phe Arg Arg Trp Asn Cys Ser Ser His Ser Lys Ala Phe Gly Arg
 60 65 70
 Ile Leu Gln Gln Gly Gln Cys Gly Glu Gly His Pro Ala Arg Thr Leu
 75 80 85
 Pro Pro Arg Pro Leu Gly Gln Pro Ser Arg Arg Arg Phe Gln Val Pro
 90 95 100
 Gly Pro Ser
 105

<210> 85

<211> 1754
 <212> DNA
 <213> Homo sapiens

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 <222> 1..117

<220>
 <221> CDS
 <222> 118..510

<220>
 <221> 3'UTR
 <222> 511..1754

<220>
 <221> polyA_signal
 <222> 1718..1723

<220>
 <221> polyA_site
 <222> 1739..1754

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<400> 85
tccccggcgc cgcgcgttgc gctcgccgcg ctgcactga agccccgggcc ctgcgcgcgc 60
gcggttcgcgc cgcgcagctc gccccctgcc caccggggcg gcctagggc ggtcacg 117
atg ctg cgc ccc tta ccc tcc cgc ctc ggg ctg ctg ctg ctg ctg ctc 165
Met Leu Pro Pro Leu Pro Ser Arg Leu Gly Leu Leu Leu Leu Leu Leu
-20 -15 -10
ctg tgc cgc gcg cac gtc ggc gga ctg tgg tgg gct gtg ggc agc ccc 213
Leu Cys Pro Ala His Val Gly Gly Leu Trp Trp Ala Val Gly Ser Pro
-5 1 5
ttg gtt atg gac cct acc agc atc tgc agg aag gca cgg cgg ctg gcc 261
Leu Val Met Asp Pro Thr Ser Ile Cys Arg Lys Ala Arg Arg Leu Ala
10 15 20 25
ggg cgg cag gcc gag ttg tgc cag gct gag cgc gaa gtg gtg gca gag 309
Gly Arg Gln Ala Glu Leu Cys Gln Ala Glu Pro Glu Val Val Ala Glu
30 35 40
ctg gct cgg ggc gcc cgg ctc ggg gtg cga gag tgc cag ttc cag ttc 357
Leu Ala Arg Gly Ala Arg Leu Gly Val Arg Glu Cys Gln Phe Gln Phe
45 50 55
cgc ttc cgc cgc tgg aat tgc tcc agc cac agc aag gcc ttt gga cgc 405
Arg Phe Arg Arg Trp Asn Cys Ser Ser His Ser Lys Ala Phe Gly Arg
60 65 70
atc ctg caa cag ggt cag tgt ggg gag ggg cac cct gca agg acc ctg 453
Ile Leu Gln Gln Gly Gln Cys Gly Glu Gly His Pro Ala Arg Thr Leu
75 80 85
cct ccc agg ccc ctg ggg cag ccc tcc cgc cgc agg ttt cag gtc cca 501
Pro Pro Arg Pro Leu Gly Gln Pro Ser Arg Arg Arg Phe Gln Val Pro
90 95 100 105
ggc ccc agc tgaccgcccc agccccgcgt gattgcacct gtctgcattc 550
Gly Pro Ser
acagacattc gggagacggc cttcgtgttc gccatcactg cggccggcgc cagccaagcc 610
gtcacgcagg cctgttctat gggcgagctg ctgcagtgcg gctgccaggc gccccgcggg 670
cgggcccctc cccggccctc cggcctgccc ggcacccccg gaacccctcg ccccgcgggc 730
tccccggaag gcagcgcgcg ctgggagttg ggaggctgcg gcgacgacgt ggaacttcggg 790
gacgagaagt cgaggctctt tatggacgcg cggcacaagc ggggacgcgg agacatccgc 850
gcgtgtgtgc aactgcacaa caacgagggc ggcaggctgg ccgtgcggag ccacacgcgc 910
accgagtgc aatgccacgg gctgtcggga tgcgcacgtg ctggcagaag 970
ctgcctccat ttgcgaggtt gggcgcgccg ctgctggagc gcttycacgg cgcttcacgc 1030
gtcatgggca ccaacgacgg caaggccctg tccgcacgct caagccgcgc 1090
ggccgagcgg acctctctta gcgcccgcat tcgcccgact tctgcgcccc caaccgacgc 1150

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accggctccc ccggcacgcg cggtcgcgcc tgcaatagca ggcggccgga cctcagcgcg 1210
tgcgacctgc tgtgctgcgg ccgcggggcac gcgcaggaga gcgtgcagct cgaagagaac 1270
tgccctgtgcc gcttccactg gtgctgcgta gtacagtgcc accgctgccg tgtgcgcaag 1330
gagctcagcc tctgctgtg acccgccgcc cgcccgctag actgaactcg cgacgcggtg 1390
gctcgcacct gtgggacctc agggcacccg caccggggcg ctctcgccgc tcgagcccgag 1450
cctctccctg ccaaagccca actcccaggg ctctgggaaat ggtgaggcga ggggcttgag 1510
aggaacgccc acccacgaag gccacggggc ccagacggcc ccgaaaaggc gtcgggggag 1570
cgtttaaagg acactgtaca ggccctccct ccccttgccc tctaggagga aacagttttt 1630
tagactggaa aaaagccagt ctaaaggcct ctggatactg ggctccccag aactgctggc 1690
cacaggatgg tgggtgaggt tagtatcaat aaagatatatt aaaccaccaa aaaaaaaaaa 1750
aaaa

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<210> 86
<211> 131
<212> PRT
<213> Homo sapiens

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<220>
<221> SIGNAL
<222> 1..24

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<400> 86
Met Leu Pro Pro Leu Pro Ser Arg Leu Gly Leu Leu Leu Leu Leu
-20 -15 -10
Leu Cys Pro Ala His Val Gly Gly Leu Trp Trp Ala Val Gly Ser Pro
-5 1 5
Leu Val Met Asp Pro Thr Ser Ile Cys Arg Lys Ala Arg Arg Leu Ala
10 15 20
Gly Arg Gln Ala Glu Leu Cys Gln Ala Glu Pro Glu Val Val Ala Glu
25 30 35 40
Leu Ala Arg Gly Ala Arg Leu Gly Val Arg Glu Cys Gln Phe Gln Phe
45 50 55
Arg Phe Arg Arg Trp Asn Cys Ser Ser His Ser Lys Ala Phe Gly Arg
60 65 70
Ile Leu Gln Gln Gly Gln Cys Gly Glu Gly His Pro Ala Arg Thr Leu
75 80 85
Pro Pro Arg Pro Leu Gly Gln Pro Ser Arg Arg Arg Phe Gln Val Pro
90 95 100
Gly Pro Ser
105

```

```

<210> 87
<211> 1431
<212> DNA
<213> Homo sapiens

```

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<220>
<221> 5'UTR
<222> 1..151

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<220>
<221> CDS
<222> 152..655

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<220>
<221> 3'UTR
<222> 656..1431

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<220>
<221> polyA_signal
<222> 1399..1404

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<220>

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<221> polyA_site

<222> 1416..1431

<400> 87

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aatTTTTtTtTt cacaaggact gggTgaagag ttctgcagcc ttacagagac tggaaaagaa 60
gcccaaaacca aggcccccag agaggTcccc caggccctt tgggtccctg agcctcagct 120
ggagatccgg cgcaggagac caacgcctgc c atg ctg ttc cgg ctg tca gag 172
Met Leu Phe Arg Leu Ser Glu
1 5
cac tcc tca cca gag gag gaa gcc tcc ccc cac cag aga gcc tca gga 220
His Ser Ser Pro Glu Glu Ala Ser Pro His Gln Arg Ala Ser Gly
10 15 20
gag ggg cac cat ctg aag tgg aag aga ccc aac ccc tgt gcc tac aca 268
Glu Gly His His Leu Lys Ser Lys Arg Pro Asn Pro Cys Ala Tyr Thr
25 30 35
cca cct tgg ctg aaa gct gtg cag cgc att gct gag tct cac ctg cag 316
Pro Pro Ser Leu Lys Ala Val Gln Arg Ile Ala Glu Ser His Leu Gln
40 45 50 55
tct atc agc aat ttg aat gag aac cag gcc tca gag gag gag gat gag 364
Ser Ile Ser Asn Leu Asn Glu Asn Gln Ala Ser Glu Glu Glu Asp Glu
60 65 70
ctg ggg gag ctt cgg gag ctg ggt tat cca aga gag gaa gat gag gag 412
Leu Gly Glu Leu Arg Glu Leu Gly Tyr Pro Arg Glu Glu Asp Glu Glu
75 80 85
gaa gag gag gat gat gaa gaa gag gaa gaa gaa gag gac agc cag gct 460
Glu Glu Glu Asp Asp Glu Glu Glu Glu Glu Glu Asp Ser Gln Ala
90 95 100
gaa gtc ctg aag gtc atc agg cag tct gct ggg caa aag aca acc tgt 508
Glu Val Leu Lys Val Ile Arg Gln Ser Ala Gly Gln Lys Thr Thr Cys
105 110 115
ggc cag ggt ctg gaa ggg ccc tgg gag cgc cca ccc cct ctg gat gag 556
Gly Gln Gly Leu Glu Gly Pro Trp Glu Arg Pro Pro Pro Leu Asp Glu
120 125 130 135
tcc gag aga gat gga ggc tct gag gac caa gtg gaa gac cca gca cta 604
Ser Glu Arg Asp Gly Gly Ser Glu Asp Gln Val Glu Asp Pro Ala Leu
140 145 150
agt gag cct ggg gag gaa cct cag cgc cct tcc ccc tct gag cct ggc 652
Ser Glu Pro Gly Glu Glu Pro Gln Arg Pro Ser Pro Ser Glu Pro Gly
155 160 165
aca taggcacca gcctgcattt cccaggagga agtggagggg acatcgtctg 705
Thr
tccccagaaa cccactctat cctcaccctg ttttgtctc ttccctctgc ctgctagggc 765
tgccggtctt gacttctaga agactaaggc tggctctgtg ttgcttgttt gccacacctt 825
ggctgatacc cagagaacct gggcacttgc tgctctgatgc ccacccctgc cagtcattcc 885
tccattcacc cagcggggagg tgggatgtga gacagccacc attggaaaat ccagaaaacc 945
gggaacaggg atttgcctt cacaattcta ctccccagat cctctccctt ggacacagga 1005
gacccacagg gcaggacct aagatctggg gaaaggagggt cctgagaacc ttgaggtacc 1065
cttagatcct tttctacca ctttctctatg gaggattcca agtcaccact tctctcaccg 1125
gcttctacca gggTccagga ctaaggcggt ttctccata gcctcaacat ttTgggaate 1185
ttcccttaat caccctgtct cctcctgggt gcctggaaga tggactggca gagacctctt 1245
tgttgcttt ttgtcttga tgccaggaat gccgcctagt ttatgtcccc ggtggggcac 1305
acagcggggg gcgccagggt ttccctgtcc cccagctgct ctgccccctt cccctctctc 1365
cctgactcca ggctgaacc cctccctgtc tgtaataaat ctttTgaaag aaaaaaaaaa 1425
aaaaaa 1431
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<210> 88

<211> 168

<212> PRT

<213> Homo sapiens

<400> 88

Met Leu Phe Arg Leu Ser Glu His Ser Ser Pro Glu Glu Glu Ala Ser
1 5 10 15

Pro His Gln Arg Ala Ser Gly Glu Gly His His Leu Lys Ser Lys Arg
 20 25 30
 Pro Asn Pro Cys Ala Tyr Thr Pro Ser Leu Lys Ala Val Gln Arg
 35 40 45
 Ile Ala Glu Ser His Leu Gln Ser Ile Ser Asn Leu Asn Glu Asn Gln
 50 55 60
 Ala Ser Glu Glu Glu Asp Glu Leu Gly Glu Leu Arg Glu Leu Gly Tyr
 65 70 75 80
 Pro Arg Glu Glu Asp Glu Glu Glu Glu Asp Glu Glu Glu Glu
 85 90 95
 Glu Glu Glu Asp Ser Gln Ala Glu Val Leu Lys Val Ile Arg Gln Ser
 100 105 110
 Ala Gly Gln Lys Thr Thr Cys Gly Gln Gly Leu Glu Gly Pro Trp Glu
 115 120 125
 Arg Pro Pro Pro Leu Asp Glu Ser Glu Arg Asp Gly Ser Glu Asp
 130 135 140
 Gln Val Glu Asp Pro Ala Leu Ser Glu Pro Gly Glu Glu Pro Gln Arg
 145 150 155 160
 Pro Ser Pro Ser Glu Pro Gly Thr
 165

<210> 89
 <211> 1431
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..151

<220>
 <221> CDS
 <222> 152..655

<220>
 <221> 3'UTR
 <222> 656..1431

<220>
 <221> polyA_signal
 <222> 1399..1404

<220>
 <221> polyA_site
 <222> 1416..1431

<400> 89
 aattttttct cacaaggact ggggtgaagag ttctgcagcc ttacagagac tggaaaagaa 60
 gcccaaacca agggcccag agaggctccc caggccctt tgggtccctg agcctcagct 120
 ggagatccgg cgcaggagac caacgcctgc c atg ctg ttc cgg ctc tca gag 172
 Met Leu Phe Arg Leu Ser Glu
 1 5
 cac tcc tca cca gag gag gaa gcc tcc ccc cac cag aga gcc tca gga 220
 His Ser Ser Pro Glu Glu Glu Ala Ser Pro His Gln Arg Ala Ser Gly
 10 15
 gag ggg cac cat ctc aag tgg aag aga ccc aac ccc tgt gcc tac aca 268
 Glu Gly His His Leu Lys Ser Lys Arg Pro Asn Pro Cys Ala Tyr Thr
 25 30 35
 cca cct tcg ctg aaa gct gtg cag cgc att gct gag tct cac ctg cag 316
 Pro Pro Ser Leu Lys Ala Val Gln Arg Ile Ala Glu Ser His Leu Gln
 40 45 50 55
 tct atc agc aat ttg aat gag aac cag gcc tca gag gag gag gat gag 364
 Ser Ile Ser Asn Leu Asn Glu Asn Gln Ala Ser Glu Glu Glu Asp Glu

<210> 91
 <211> 1417
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..47

<220>
 <221> CDS
 <222> 48..1301

<220>
 <221> 3'UTR
 <222> 1302..1417

<220>
 <221> polyA_signal
 <222> 1360..1365

<220>
 <221> polyA_site
 <222> 1402..1417

<400> 91
 ctcctcagct tcaggcacca ccactgacct gggacagtga atcgaca atg ccg tct 56
 Met Pro Ser
 tct gtc tcg tgg ggc atc ctc ctg ctg gca ggc ctg tgc tgc ctg gtc 104
 Ser Val Ser Trp Gly Ile Leu Leu Leu Ala Gly Leu Cys Cys Leu Val
 -20 -15 -10 -5
 cct gtc tcc ctg gct gag gat ccc cag gga gat gct gcc cag aag aca 152
 Pro Val Ser Leu Ala Glu Asp Pro Gln Gly Asp Ala Ala Gln Lys Thr
 1 5 10
 gat aca tcc cac cat gat cag gat cac cca acc ttc aac aag atc acc 200
 Asp Thr Ser His His Asp Gln Asp His Pro Thr Phe Asn Lys Ile Thr
 15 20 25
 ccc aac ctg gct gag ttc gcc ttc agc cta tac cgc cag ctg gca cac 248
 Pro Asn Leu Ala Glu Phe Ala Phe Ser Leu Tyr Arg Gln Leu Ala His
 30 35 40
 cag tcc aac agc acc aat atc ttc ttc tcc cca gtg agc atc gct aca 296
 Gln Ser Asn Ser Thr Asn Ile Phe Phe Ser Pro Val Ser Ile Ala Thr
 45 50 55 60
 gcc ttt gca atg ctc tcc ctg ggg acc aag gct gac act cac gat gaa 344
 Ala Phe Ala Met Leu Ser Leu Gly Thr Lys Ala Asp Thr His Asp Glu
 65 70 75
 atc ctg gag agc ctg aat ttc aac ctc acg gag att ccg gag gct cag 392
 Ile Leu Glu Ser Leu Asn Phe Asn Leu Thr Glu Ile Pro Glu Ala Gln
 80 85 90
 atc cat gaa ggc ttc cag gaa ctc ctc cgt acc ctc aac cag cca gac 440
 Ile His Glu Gly Phe Gln Glu Leu Leu Arg Thr Leu Asn Gln Pro Asp
 95 100 105
 agc cag ctc cag ctg acc acc ggc aat ggc ctg ttc ctc agc gag ggc 488
 Ser Gln Leu Gln Leu Thr Thr Gly Asn Gly Leu Phe Leu Ser Glu Gly
 110 115 120
 ctg aag cta gtg gat aag ttt ttg gag gat gtt aaa aag ttg tac cac 536
 Leu Lys Leu Val Asp Lys Phe Leu Glu Asp Val Lys Lys Leu Tyr His
 125 130 135 140
 tca gaa gcc ttc act gtc aac ttc ggg gac acc gaa gag gcc aag aaa 584
 Ser Glu Ala Phe Thr Val Asn Phe Gly Asp Thr Glu Glu Ala Lys Lys
 145 150 155
 cag atc aac gat tac gtg gag aag ggt act caa ggg aaa att gtg gat 632

Gln Ile Asn Asp Tyr Val Glu Lys Gly Thr Gln Gly Lys Ile Val Asp	
160 165 170	
ttg gtc aag gag ctt gac aga gac aca gtt ttt gct ctg gtc aat tac	680
Leu Val Lys Glu Leu Asp Arg Asp Thr Val Phe Ala Leu Val Asn Tyr	
175 180 185	
atc ttc ttt aaa ggc aaa tgg gag aga ccc ttt gaa gtc aag gac acc	728
Ile Phe Phe Lys Gly Lys Trp Glu Arg Pro Phe Glu Val Lys Asp Thr	
190 195 200	
gag gaa gag gac ttc cac gtc gac cag gcg acc acc gtc aag gtc cct	776
Glu Glu Glu Asp Phe His Val Asp Gln Ala Thr Thr Val Lys Val Pro	
205 210 215	
atg atg aag cgt tta ggc atg ttt aac atc cag cac tgt aag aag ctg	824
Met Met Lys Arg Leu Gly Met Phe Asn Ile Gln His Cys Lys Leu	
225 230 235	
tcc agc tgg gtc ctg ctg atg aaa tac ctg ggc aat gcc acc gcc atc	872
Ser Ser Trp Val Leu Leu Met Lys Tyr Leu Gly Asn Ala Thr Ala Ile	
240 245 250	
ttc ttc ctg cct gat gag ggg aaa cta cag cac ctg gaa aat gaa ctc	920
Phe Phe Leu Pro Asp Glu Gly Lys Leu Gln His Leu Glu Asn Glu Leu	
255 260 265	
acc cac gat atc atc acc aag ttc ctg gaa aat gaa gac aga agg tct	968
Thr His Asp Ile Ile Thr Lys Phe Leu Glu Asn Glu Asp Arg Arg Ser	
270 275 280	
gcc agc tta cat tta ccc aaa ctg tcc att act gga acc tat gat ctg	1016
Ala Ser Leu His Leu Pro Lys Leu Ser Ile Thr Gly Thr Tyr Asp Leu	
285 290 295	
aag agc gtc ctg ggt caa ctg ggc atc act aag gtc ttc agc aat ggg	1064
Lys Ser Val Leu Gly Gln Leu Gly Ile Thr Lys Val Phe Ser Asn Gly	
305 310 315	
gct gac ctc tcc ggg gtc aca gag gag gca ccc ctg aag ctc tcc aag	1112
Ala Asp Leu Ser Glu Gly Val Thr Glu Glu Ala Pro Leu Lys Leu Ser Lys	
320 325 330	
gcc gtc cat aag gct gtc ctg acc atc gac gag aaa ggg act gaa gct	1160
Ala Val His Lys Ala Val Leu Thr Ile Asp Glu Lys Gly Thr Glu Ala	
335 340 345	
gct ggg gcc atg ttt tta gag gcc ata ccc atg tct atc ccc ccc gag	1208
Ala Gly Ala Met Phe Leu Glu Ala Ile Pro Met Ser Ile Pro Pro Glu	
350 355 360	
gtc aag ttc aac aaa ccc ttt gtc ttc tta atg att gaa caa aat acc	1256
Val Lys Phe Asn Lys Pro Phe Val Phe Leu Met Ile Glu Gln Asn Thr	
365 370 375	
aag tct ccc ctc ttc atg gga aaa gtc gtc aat ccc acc caa aaa	1301
Lys Ser Pro Leu Phe Met Gly Lys Val Val Asn Pro Thr Gln Lys	
385 390 395	
taactgcctc togtctctca acccctcccc tccatccctg gccccctccc tggatgacat	1361
taaaagaagg ttgagctggt cccctgcctgc atgtgactgc aaaaaaaaaa aaaaaa	1417

<210> 92

<211> 418

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> 1..24

<400> 92

Met Pro Ser Ser Val Ser Trp Gly Ile Leu Leu Leu Ala Gly Leu Cys

-20 -15 -10

Cys Leu Val Pro Val Ser Leu Ala Glu Asp Pro Gln Gly Asp Ala Ala

-5 1 5

Gln Lys Thr Asp Thr Ser His His Asp Gln Asp His Pro Thr Phe Asn

10 15 20

Lys Ile Thr Pro Asn Leu Ala Glu Phe Ala Phe Ser Leu Tyr Arg Gln
 25 30 35 40
 Leu Ala His Gln Ser Asn Ser Thr Asn Ile Phe Phe Ser Pro Val Ser
 45 50 55
 Ile Ala Thr Ala Phe Ala Met Leu Ser Leu Gly Thr Lys Ala Asp Thr
 60 65 70
 His Asp Glu Ile Leu Glu Ser Leu Asn Phe Asn Leu Thr Glu Ile Pro
 75 80 85
 Glu Ala Gln Ile His Glu Gly Phe Gln Glu Leu Leu Arg Thr Leu Asn
 90 95 100
 Gln Pro Asp Ser Gln Leu Gln Leu Thr Thr Gly Asn Gly Leu Phe Leu
 105 110 115 120
 Ser Glu Gly Leu Lys Leu Val Asp Lys Phe Leu Glu Asp Val Lys Lys
 125 130 135
 Leu Tyr His Ser Glu Ala Phe Thr Val Asn Phe Gly Asp Thr Glu Glu
 140 145 150
 Ala Lys Lys Gln Ile Asn Asp Tyr Val Glu Lys Gly Thr Gln Gly Lys
 155 160 165
 Ile Val Asp Leu Val Lys Glu Leu Asp Arg Asp Thr Val Phe Ala Leu
 170 175 180
 Val Asn Tyr Ile Phe Phe Lys Gly Lys Trp Glu Arg Pro Phe Glu Val
 185 190 195 200
 Lys Asp Thr Glu Glu Glu Asp Phe His Val Asp Gln Ala Thr Thr Val
 205 210 215
 Lys Val Pro Met Met Lys Arg Leu Gly Met Phe Asn Ile Gln His Cys
 220 225 230
 Lys Lys Leu Ser Ser Trp Val Leu Leu Met Lys Tyr Leu Gly Asn Ala
 235 240 245
 Thr Ala Ile Phe Phe Leu Pro Asp Glu Gly Lys Leu Gln His Leu Glu
 250 255 260
 Asn Glu Leu Thr His Asp Ile Ile Thr Lys Phe Leu Glu Asn Glu Asp
 265 270 275 280
 Arg Arg Ser Ala Ser Leu His Leu Pro Lys Leu Ser Ile Thr Gly Thr
 285 290 295
 Tyr Asp Leu Lys Ser Val Leu Gly Gln Leu Gly Ile Thr Lys Val Phe
 300 305 310
 Ser Asn Gln Ala Asp Leu Ser Gly Val Thr Glu Glu Ala Pro Leu Lys
 315 320 325
 Leu Ser Lys Ala Val His Lys Ala Val Leu Thr Ile Asp Glu Lys Gly
 330 335 340
 Thr Glu Ala Ala Gly Ala Met Phe Leu Glu Ala Ile Pro Met Ser Ile
 345 350 355 360
 Pro Pro Glu Val Lys Phe Asn Lys Pro Phe Val Phe Leu Met Ile Glu
 365 370 375
 Gln Asn Thr Lys Ser Pro Leu Phe Met Gly Lys Val Val Asn Pro Thr
 380 385 390
 Gln Lys

<210> 93
 <211> 1115
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..277

<220>
 <221> CDS
 <222> 278..733

<220>
 <221> 3'UTR

<222> 734..1115

<220>

<221> polyA_signal

<222> 1072..1077

<220>

<221> polyA_site

<222> 1101..1115

<400> 93

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ctctttcact gctagtaaga tcagattgcg ttcttttcag ttaactttca atcgccagtt 120
tcttgatctg cttctaaaag aagaagtaga gaagataaat cctgtcttca atacctggaa 180
ggaaaaacaa aataacctca actccgcttt gaaaaaaaca ttccaagaac ttctatcaga 240
gattttactt agatgattta cacaatgaag aaagtac atg cac ttt ggg ctt ctg 295
Met His Phe Gly Leu Leu
-15
tcc ctg ctg ctt aat ctt gcc cct gcc cct ctt aat gct gat tct gag 343
Ser Leu Leu Leu Asn Leu Ala Pro Ala Pro Leu Asn Ala Asp Ser Glu
-10 -5 1
gaa gat gaa gaa cac aca att atc aca gat acg gag ttg cca cca ctg 391
Glu Asp Glu Glu His Thr Ile Ile Thr Asp Thr Glu Leu Pro Pro Leu
5 10 15 20
aaa ctt atg cat tca ttt tgt gca ttc aag gcg gat gat agc cca tgt 439
Lys Leu Met His Ser Phe Cys Ala Phe Lys Ala Asp Asp Ser Pro Cys
25 30 35
aaa gca atc atg aaa aga ttt ttc ttc aat att ttc act cga cag tgc 487
Lys Ala Ile Met Lys Arg Phe Phe Phe Asn Ile Phe Thr Arg Gln Cys
40 45 50
gaa gaa ttt ata tat ggg gga tgt gaa gga aat cag aat cga ttt gaa 535
Glu Glu Phe Ile Tyr Gly Gly Cys Glu Gly Asn Gln Asn Arg Phe Glu
55 60 65
agt ctg gaa gag tgc aaa aaa atg tgt aca aga gat aat gca aac agg 583
Ser Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Asp Asn Ala Asn Arg
70 75 80
att ata aag aca aca ttg caa caa gaa aag cca gat ttc tgc ttt ttg 631
Ile Ile Lys Thr Thr Leu Gln Gln Glu Lys Pro Asp Phe Cys Phe Leu
85 90 95 100
gaa gaa gat cct gga ata tgt cga ggt tat att acc agg tat ttt tat 679
Glu Glu Asp Pro Gly Ile Cys Arg Gly Tyr Ile Thr Arg Tyr Phe Tyr
105 110 115
aac aat cag aca aaa cat gtg aac gtt tca agt atg gtg gat gcc tgg 727
Asn Asn Gln Thr Lys His Val Asn Val Ser Ser Met Val Asp Ala Trp
120 125 130
gca ata tgaacaattt tgagacactg gaagaatgca agaacatttg tgaagatggt 783
Ala Ile
ccgaatggtt tccaggtgga taattatgga acccagctca atgctgtgaa taactccctg 843
actccgcaat caaccaaggt tcccagcctt ttgttacaa aagaaggaac aaatgatggt 903
tggaagaatg cggctcatat ttaccaagtc tttctgaacg cctttctgcat tcatgcatcc 963
atgttctttc taggattgga tagcatttca tgcctatggt aatatttgtg cttttggcat 1023
ttccttaata tttatatgta tacgtgatgc ctttgatagc atactgctaa taaagtttta 1083
atatttcat gcataggaaa aaaaaaaaaa aa 1115
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<210> 94

<211> 152

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> 1..19

<210> 97
 <211> 1855
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..117

<220>
 <221> CDS
 <222> 118..504

<220>
 <221> 3'UTR
 <222> 505..1855

<220>
 <221> polyA_signal
 <222> 1819..1824

<220>
 <221> polyA_site
 <222> 1840..1855

<400> 97
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 ggcgttgcgc cgcgcgcctc gccccctgcc caccggggcg gcctgaggcg ggtcacg 117
 atg ctg cgc ccc tta ccc tcc cgc ctc ggg ctg ctg ctg ctg ctg ctc 165
 Met Leu Pro Pro Leu Pro Ser Arg Leu Gly Leu Leu Leu Leu Leu
 -20 -15 -10
 ctg tgc cgc gcg cac gtc ggc gga ctg tgg tgg gct gtg ggc agc ccc 213
 Leu Cys Pro Ala His Val Gly Gly Leu Trp Trp Ala Val Gly Ser Pro
 -5 1 5
 ttg gtt atg gac cct acc agc atc tgc agg aag gca cgg cgg ctg gcc 261
 Leu Val Met Asp Pro Thr Ser Ile Cys Arg Lys Ala Arg Arg Leu Ala
 10 15 20 25
 ggg cgg cag gcc gag ttg tgc cag gct gag cgc gaa gtg gtg gca gag 309
 Gly Arg Gln Ala Glu Leu Cys Gln Ala Glu Pro Glu Val Val Ala Glu
 30 35 40
 ctg gct cgg ggc gcc cgg ctc ggg gtg cga gag tgc cag ttc cag ttc 357
 Leu Ala Arg Gly Ala Arg Leu Gly Val Arg Glu Cys Gln Phe Gln Phe
 45 50 55
 cgc ttc cgc cgc tgg aat tgc tcc agc cac agc aag gcc ttt gga cgc 405
 Arg Phe Arg Arg Trp Asn Cys Ser Ser His Ser Lys Ala Phe Gly Arg
 60 65 70
 atc ctg caa cag ggt cag tgt ggg gag ggg gcg gaa gtg ggg ctg ctt 453
 Ile Leu Gln Gln Gly Gln Cys Gly Glu Gly Ala Glu Val Gly Leu Leu
 75 80 85
 tct ccc tgc tgt ggg acc cga gga gag gag aac tgg ttc gct gaa gtt 501
 Ser Pro Cys Cys Gly Thr Arg Gly Glu Glu Asn Trp Phe Ala Glu Val
 90 95 100 105
 gcc tgagccccca ttccccctca catgtgtctg ggcacctgc aaggacctg 554
 Ala
 cctccccagg cctctggggc gccctccgcg cgcaggttcc aggtccccagg ccccgactga 614
 cgcgccagc cgcgcgtgat tgcacctgtc tgcattcaca gacattcggg agacggcctt 674
 cgtgttgcgc atcactgcgg cgcggcccgag ccacgcgcct acgcaggcct gttctatggg 734
 cagctcgtc cagtgcggct gccaggcgcc cgcgcggcgg gccctcccc gccctccgg 794
 cctgcccgcc acccccggac cccctggccc cgcgggctcc ccggaaggca gcgcgcctg 854
 gaagtgggga ggctgcggcg acgacgtgga cttcggggac gagaagtcga ggctctttat 914
 ggacgcgcgg cacaagcggg gacgcggaga catccgcgcg ttggtgcaac tgcacaacaa 974

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cgagcgcgggc aggcgtggccg tgcggagcca cagcgccacc gaggcgcaaat gccacgggct 1034
gtcgggatca tgcgcgctgc gcacctgctg gcagaagctg cctccatttc gccaggtggg 1094
cgcgcggtctg ctggagcgct tccacggcgc ctccacgctc atgggaccca acgacgggcaa 1154
ggccctgtctg cccgcgctcc gcacgctcaa gccgcgggc cgagcggacc tcctctacgc 1214
gcgcgattcg cccgacttct gcgcccccaa ccgacgcacc ggctcccccg gcacgcgcgg 1274
cgcgcgctgc aatagcagcg ccccggaact cagcggtgct gacctgctgt gctgcggccg 1334
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gcacccggc cgggcgcctc tcgcccgtcg agccccagcct ctccctgcca aagcccaact 1574
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caggcgccca gacggccccc aaaaggcgct cggggagcgt ttaaaggaca ctgtacaggc 1694
cctccctcc cctgcccctc aggaggaaac agtttttttag actggaaaaa agccagtcta 1754
aaggcctctg gatactgggc tccccagaac tgctggccac aggatgggtg gtgaggttag 1814
tatcaataaa gatatttaa ccacaaaaaa aaaaaaaaaa a 1855

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<210> 98
<211> 129
<212> PRT
<213> Homo sapiens

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<220>
<221> SIGNAL
<222> 1..24

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<400> 98
Met Leu Pro Pro Leu Pro Ser Arg Leu Gly Leu Leu Leu Leu Leu
          -20          -15          -10
Leu Cys Pro Ala His Val Gly Gly Leu Trp Trp Ala Val Gly Ser Pro
          -5          1          5
Leu Val Met Asp Pro Thr Ser Ile Cys Arg Lys Ala Arg Arg Leu Ala
          10          15          20
Gly Arg Gln Ala Glu Leu Cys Gln Ala Glu Pro Glu Val Val Ala Glu
          25          30          35          40
Leu Ala Arg Gly Ala Arg Leu Gly Val Arg Glu Cys Gln Phe Gln Phe
          45          50          55
Arg Phe Arg Arg Trp Asn Cys Ser Ser His Ser Lys Ala Phe Gly Arg
          60          65          70
Ile Leu Gln Gln Gly Gln Cys Gly Glu Gly Ala Glu Val Gly Leu Leu
          75          80          85
Ser Pro Cys Cys Gly Thr Arg Gly Glu Glu Asn Trp Phe Ala Glu Val
          90          95          100
Ala
105

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<210> 99
<211> 667
<212> DNA
<213> Homo sapiens

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<220>
<221> 5'UTR
<222> 1..94

<220>
<221> CDS
<222> 95..613

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<220>
<221> 3'UTR
<222> 614..667

<220>

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<221> polyA_signal

<222> 636..641

<220>

<221> polyA_site

<222> 652..667

<400> 99

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gttccatctc aacagccctt gttttggaaa ggac atg att gtc aag ggg gtg gcc 115
                               Met Ile Val Lys Gly Val Ala
                               1           5
tcc aga act gtg gtt tcc aga cgc ttc ccc ggt aac tgg ctt ttc tct 163
Ser Arg Thr Val Val Ser Arg Pro Phe Pro Gly Asn Trp Leu Phe Ser
                               10          15          20
tcc atc cag ctg act gat gat cag ggc ccc gtc ctg atg acc act gta 211
Ser Ile Gln Leu Thr Asp Asp Gln Gly Pro Val Leu Met Thr Thr Val
                               25          30          35
gcc atg cct gtg ttt agt aag cag aac gaa acc aga tcg aag ggc att 259
Ala Met Pro Val Phe Ser Lys Gln Asn Glu Thr Arg Ser Lys Gly Ile
                               40          45          50          55
ctt ctg gga gtg gtt ggc aca gat gtc cca gtg aaa gaa ctt ctg aag 307
Leu Leu Gly Val Val Gly Thr Asp Val Pro Val Lys Glu Leu Leu Lys
                               60          65          70
acc atc ccc aaa tac aag tta ggg att cac ggt tat gcc ttt gca atc 355
Thr Ile Pro Lys Tyr Lys Leu Gly Ile His Gly Tyr Ala Phe Ala Ile
                               75          80          85
aca aat aat gga tat atc ctg acg cat ccg gaa ctc agg ctg ctg tac 403
Thr Asn Asn Gly Tyr Ile Leu Thr His Pro Glu Leu Arg Leu Leu Tyr
                               90          95          100
gaa gaa gga aaa aag cga agg aaa cct aac tat agt agc gtt gac ctc 451
Glu Glu Gly Lys Lys Arg Arg Lys Pro Asn Tyr Ser Ser Val Asp Leu
                               105          110          115
tct gag gtg gag tgg gaa gac cga gat gac gtg ttg aga aat gct atg 499
Ser Glu Val Glu Trp Glu Asp Arg Asp Asp Val Leu Arg Asn Ala Met
                               120          125          130          135
gtg aat cga aag acg ggg aag ttt tcc atg gag gtg aag aag aca gtg 547
Val Asn Arg Lys Thr Gly Lys Phe Ser Met Glu Val Lys Lys Thr Val
                               140          145          150
gac aaa ggg gta cat ttt tct caa aca ttt ttg ctg ctt aat tta aaa 595
Asp Lys Gly Val His Phe Ser Gln Thr Phe Leu Leu Leu Asn Leu Lys
                               155          160          165
caa acc act gtg aaa aat tagctttgaa agctatatct ggaataaata 643
Gln Thr Thr Val Lys Asn
                               170
tccttcgcga aaaaaaaaaa aaaa 667
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<210> 100

<211> 173

<212> PRT

<213> Homo sapiens

<400> 100

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Met Ile Val Lys Gly Val Ala Ser Arg Thr Val Val Ser Arg Pro Phe
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Pro Gly Asn Trp Leu Phe Ser Ser Ile Gln Leu Thr Asp Asp Gln Gly
                20          25          30
Pro Val Leu Met Thr Thr Val Ala Met Pro Val Phe Ser Lys Gln Asn
                35          40          45
Glu Thr Arg Ser Lys Gly Ile Leu Leu Gly Val Val Gly Thr Asp Val
                50          55          60
Pro Val Lys Glu Leu Leu Lys Thr Ile Pro Lys Tyr Lys Leu Gly Ile
                65          70          75          80
```

His Gly Tyr Ala Phe Ala Ile Thr Asn Asn Gly Tyr Ile Leu Thr His
 85 90 95
 Pro Glu Leu Arg Leu Leu Tyr Glu Glu Gly Lys Lys Arg Arg Lys Pro
 100 105 110
 Asn Tyr Ser Ser Val Asp Leu Ser Glu Val Glu Trp Glu Asp Arg Asp
 115 120 125
 Asp Val Leu Arg Asn Ala Met Val Asn Arg Lys Thr Gly Lys Phe Ser
 130 135 140
 Met Glu Val Lys Lys Thr Val Asp Lys Gly Val His Phe Ser Gln Thr
 145 150 155 160
 Phe Leu Leu Leu Asn Leu Lys Gln Thr Thr Val Lys Asn
 165 170

<210> 101
 <211> 1062
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..153

<220>
 <221> CDS
 <222> 154..639

<220>
 <221> 3'UTR
 <222> 640..1062

<220>
 <221> polyA_signal
 <222> 1023..1028

<220>
 <221> polyA_site
 <222> 1047..1062

<400> 101
 attggtgtat ggcttttcag caataactga tggctgtttc cctcctgct tttatctttca 60
 gttaatgacc agccacggcg tccctgctgt gagctctggc cgctgccttc cagggctccc 120
 gagccacacg ctgggggtgc tggctgaggg aac atg gct tgt tgg cct cag ctg 174
 Met Ala Cys Trp Pro Gln Leu
 1 5
 agg ttg ctg ctg tgg aag aac ctc act ttc aga aga aga caa aca tgt 222
 Arg Leu Leu Leu Trp Lys Asn Leu Thr Phe Arg Arg Arg Gln Thr Cys
 10 15 20
 cag ctg ctg ctg gaa gtg gcc tgg cct cta ttt atc ttc ctg atc ctg 270
 Gln Leu Leu Leu Glu Val Ala Trp Pro Leu Phe Ile Phe Leu Ile Leu
 25 30 35
 atc tct gtt cgg ctg agc tac cca ccc tat gaa caa cat gaa tgc cat 318
 Ile Ser Val Arg Leu Ser Tyr Pro Pro Tyr Glu Gln His Glu Cys His
 40 45 50 55
 ttt cca aat aaa gcc atg ccc tct gca gga aca ctt cct tgg gtt cag 366
 Phe Pro Asn Lys Ala Met Pro Ser Ala Gly Thr Leu Pro Trp Val Gln
 60 65 70
 ggg att atc tgt aat gcc aac aac ccc tgt ttc cgt tac ccg act cct 414
 Gly Ile Ile Cys Asn Ala Asn Asn Pro Cys Phe Arg Tyr Pro Thr Pro
 75 80 85
 ggg gag gct ccc gga gtt gtt gga aac ttt aac aaa tcc att gtg gct 462
 Gly Glu Ala Pro Gly Val Val Gly Asn Phe Asn Lys Ser Ile Val Ala
 90 95 100
 cgc ctg ttc tca gat gct cgg agg ctt ctt tta tac agc cag aaa gac 510

Arg	Leu	Phe	Ser	Asp	Ala	Arg	Arg	Leu	Leu	Leu	Tyr	Ser	Gln	Lys	Asp		
105						110					115						
acc	agc	atg	aag	gac	atg	cgc	aaa	gtt	ctg	aga	aca	tta	cag	cag	atc	558	
Thr	Ser	Met	Lys	Asp	Met	Arg	Lys	Val	Leu	Arg	Thr	Leu	Gln	Gln	Ile		
120						125					130				135		
aag	aaa	tcc	agc	tca	aga	ggg	gac	aaa	cgc	cat	ttc	ctc	aac	tg	gag	606	
Lys	Lys	Ser	Ser	Ser	Arg	Gly	Asp	Lys	Arg	His	Phe	Leu	Asn	Trp	Gln		
					140				145				150				
aag	gga	ctg	aag	cct	ctc	cct	caa	gcc	ctt	tta	taggggtcct	cattgtcagg				659	
Lys	Gly	Leu	Lys	Pro	Leu	Pro	Gln	Ala	Leu	Leu							
			155				160										
cctctaaagcc	caagccaagc	catcgcatcc	cctgtgactt	gcacatatac	gcccagatgg											719	
cctgaagtaa	ctgaagaatc	acaaaagaag	tgaaaaggcc	ctgcctcgcc	ttactgatg											779	
acgtttccacc	attgtgattt	gttctgtccc	caccttaact	gagtgattaa	ccctgtgaat											839	
ttcctctctcc	tggtctcagaa	gtcctccccc	tgagcacctt	gtgaccccct	gcccctgccc											899	
accagagaac	aacccccctt	gactgttaatt	ttccattacc	ttcccaaatc	ctataaaacg											959	
gccccacccc	tatctccctt	tgctgactct	cttttcggac	tcagccccacc	tcgagccagg											1019	
tgaaaaaac	agctttattg	ctcacacaaa	aaaaaaaaaa	aaa												1062	

<210> 102
 <211> 162
 <212> PRT
 <213> Homo sapiens

<400>	102																
Met	Ala	Cys	Trp	Pro	Gln	Leu	Arg	Leu	Leu	Leu	Trp	Lys	Asn	Leu	Thr		
1				5					10					15			
Phe	Arg	Arg	Arg	Gln	Thr	Cys	Gln	Leu	Leu	Leu	Glu	Val	Ala	Trp	Pro		
				20				25					30				
Leu	Phe	Ile	Phe	Leu	Ile	Leu	Ile	Ser	Val	Arg	Leu	Ser	Tyr	Pro	Pro		
				35			40					45					
Tyr	Glu	Gln	His	Glu	Cys	His	Phe	Pro	Asn	Lys	Ala	Met	Pro	Ser	Ala		
				50		55					60						
Gly	Thr	Leu	Pro	Trp	Val	Gln	Gly	Ile	Ile	Cys	Asn	Ala	Asn	Asn	Pro		
65				70					75					80			
Cys	Phe	Arg	Tyr	Pro	Thr	Pro	Gly	Glu	Ala	Pro	Gly	Val	Val	Gly	Asn		
				85				90						95			
Phe	Asn	Lys	Ser	Ile	Val	Ala	Arg	Leu	Phe	Ser	Asp	Ala	Arg	Arg	Leu		
			100				105					110					
Leu	Leu	Tyr	Ser	Gln	Lys	Asp	Thr	Ser	Met	Lys	Asp	Met	Arg	Lys	Val		
			115			120					125						
Leu	Arg	Thr	Leu	Gln	Gln	Ile	Lys	Lys	Ser	Ser	Ser	Arg	Gly	Asp	Lys		
			130			135					140						
Arg	His	Phe	Leu	Asn	Trp	Gln	Lys	Gly	Leu	Lys	Pro	Leu	Pro	Gln	Ala		
145				150					155					160			
Leu	Leu																

<210> 103
 <211> 933
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..149

<220>
 <221> CDS
 <222> 150..392

<220>
 <221> 3'UTR
 <222> 393..933

<220>
 <221> polyA_site
 <222> 63..933

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<400> 103
aaacctctcag ggaccttgta tagacgcaga atctgtttca cacaacaact gctatttgaa 60
ggaaaaaaaaa aaaaagaagc aaatgatacc aagacaagct cataacagag atccaatcag 120
cagatgtgta cggatgaaaa tacagttag atg agt cag aaa ccg gcc aag gag 173
                                Met Ser Gln Lys Pro Ala Lys Glu
                                1          5
ggt ccc aga ctc tcc aaa aac cag aag tac tcc gaa cac ttc agc ata 221
Gly Pro Arg Leu Ser Lys Asn Gln Lys Tyr Ser Glu His Phe Ser Ile
                                10          15          20
cac tgc tgc ccg ccg ttc acc ttc ctc aat tcc aag aag gag ata gtg 269
His Cys Cys Pro Pro Phe Thr Phe Leu Asn Ser Lys Lys Glu Ile Val
                                25          30          35          40
gat cgg aaa tac agc atc tgt aag agc gcc tgc ttc tac cag aag aaa 317
Asp Arg Lys Tyr Ser Ile Cys Lys Ser Gly Cys Phe Tyr Gln Lys Lys
                                45          50          55
gag gag gac tgg atc tgc tgc gcc tgc cag aag acc aga ttg aaa agg 365
Glu Glu Asp Trp Ile Cys Cys Ala Cys Gln Lys Thr Arg Leu Lys Arg
                                60          65          70
aag atc agg cca acc cca aag aag aag tgaccaagga ggagtttaaa 412
Lys Ile Arg Pro Thr Pro Lys Lys Lys
                                75          80
ytgaatgaac aacctcggct cctggactca ttgcttcaca acccatctac cctcggatga 472
agttatctgg cttcaaatat tatgcagggg caaacacctg ctgatgtggc aactgctgat 532
gctcatgttc cccatggcat gggggcctca gggcagcctg cctggagtac ttgaaagatg 592
tcctccatt gtctctgtac ctctataatt gccactgaga gatctgctgt cagtctgctt 652
atccttccac ggaactcaagt ttcttcaatc tgaagataca tgttcttctc caaggacatg 712
tggaaaaaaa aaagatgtta tacaaccatc aaagtggcaa aaataaaaaa aattggctgg 772
gctggtgtggc gggcgctctgt ggtcccagct actcgggagg ctgaggcagg agaattggcg 832
gaacctggga ggcggagctt gcagttagcc gagatgcac cactgcactc cagcctgggc 892
gacagagcga gactctgtct caaacaacaaa aaaaaaaaaa a 933

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<210> 104
 <211> 81
 <212> PRT
 <213> Homo sapiens

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<400> 104
Met Ser Gln Lys Pro Ala Lys Glu Gly Pro Arg Leu Ser Lys Asn Gln
1          5          10          15
Lys Tyr Ser Glu His Phe Ser Ile His Cys Cys Pro Pro Phe Thr Phe
                                20          25          30
Leu Asn Ser Lys Lys Glu Ile Val Asp Arg Lys Tyr Ser Ile Cys Lys
                                35          40          45
Ser Gly Cys Phe Tyr Gln Lys Lys Glu Glu Asp Trp Ile Cys Cys Ala
                                50          55          60
Cys Gln Lys Thr Arg Leu Lys Arg Lys Ile Arg Pro Thr Pro Lys Lys
                                65          70          75          80
Lys

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<210> 105
 <211> 1187
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..34

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<220>
<221> CDS
<222> 35..1069

<220>
<221> 3'UTR
<222> 1070..1187

<220>
<221> polyA_signal
<222> 1146..1151

<220>
<221> polyA_site
<222> 1172..1187

<400> 105
accactttgg tagtgccagt gtgactcacc caca atg att tct cca gtg ctc atc 55
Met Ile Ser Pro Val Leu Ile
-15
ttg ttc tcg agt ttt ctc tgc cat gtt gct att gca gga cgg acc tgt 103
Leu Phe Ser Ser Phe Leu Cys His Val Ala Ile Ala Gly Arg Thr Cys
-10 -5 1 5
ccc aag cca gat gat tta cca ttt tcc aca gtg gtc ccg tta aaa aca 151
Pro Lys Pro Asp Asp Leu Pro Phe Ser Thr Val Val Pro Leu Lys Thr
10 15 20
ttc tat gag cca gga gaa gag att acg tat tcc tgc aag ccg ggc tat 199
Phe Tyr Glu Pro Gly Glu Glu Ile Thr Tyr Ser Cys Lys Pro Gly Tyr
25 30 35
gtg tcc cga gga ggg atg aga aag ttt atc tgc cct ctc aca gga ctg 247
Val Ser Arg Gly Met Arg Lys Phe Ile Cys Pro Leu Thr Gly Leu
40 45 50
tgg ctc atc aac act ctg aaa tgt aca ccc aga gta tgt cct ttt gct 295
Trp Leu Ile Asn Thr Leu Lys Cys Thr Pro Arg Val Cys Pro Phe Ala
55 60 65
gga atc tta gaa aat gga gcc gta cgc tat acg act ttt gaa tat ccc 343
Gly Ile Leu Glu Asn Gly Ala Val Arg Tyr Thr Thr Phe Glu Tyr Pro
70 75 80 85
aac acg atc agt ttt tct tgt aac act ggg ttt tat ctg aat ggc gct 391
Asn Thr Ile Ser Phe Ser Cys Asn Thr Gly Phe Tyr Leu Asn Gly Ala
90 95 100
gat tct gcc aag tgc act gag gaa gga aaa tgg agc ccg gag ctt cct 439
Asp Ser Ala Lys Cys Thr Glu Glu Gly Lys Trp Ser Pro Glu Leu Pro
105 110 115
gtc tgt gct ccc atc atc tgc cct cca cca tcc ata cct acg ttt gca 487
Val Cys Ala Pro Ile Ile Cys Pro Pro Pro Ser Ile Pro Thr Phe Ala
120 125 130
aca ctt cgt gtt tat aag cca tca gct gga aac aat tcc ctc tat cgg 535
Thr Leu Arg Val Tyr Lys Pro Ser Ala Gly Asn Asn Ser Leu Tyr Arg
135 140 145
gac aca gca gtt ttt gaa tgt ttg cca caa cat gcg atg ttt gga aat 583
Asp Thr Ala Val Phe Glu Cys Leu Pro Gln His Ala Met Phe Gly Asn
150 155 160 165
gat aca att acc tgc acg aca cat gga aat tgg act aaa tta cca gaa 631
Asp Thr Ile Thr Cys Thr Thr His Gly Asn Trp Thr Lys Leu Pro Glu
170 175 180
tgc agg gaa gta aaa tgc cca ttc cca tca aga cca gac aat gga ttt 679
Cys Arg Glu Val Lys Cys Pro Phe Pro Ser Arg Pro Asp Asn Gly Phe
185 190 195
gtg aac tat cct gca aaa cca aca ctt tat tac aag gat aaa gcc aca 727
Val Asn Tyr Pro Ala Lys Pro Thr Leu Tyr Tyr Lys Asp Lys Ala Thr
200 205 210
ttt ggc tgc cat gat gga tat tct ctg gat ggc ccg gaa gaa ata gaa 775

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Phe Gly Cys His Asp Gly Tyr Ser Leu Asp Gly Pro Glu Glu Ile Glu
 215 220 225
 tgt acc aaa ctg gga aac tgg tct gcc atg cca agt tgt aaa gca tct 823
 Cys Thr Lys Leu Gly Asn Trp Ser Ala Met Pro Ser Cys Lys Ala Ser
 230 235 240 245
 tgt aaa gta cct gtg aaa aaa gcc act gtg gtg tac caa gga gag aga 871
 Cys Lys Val Pro Val Lys Lys Ala Thr Val Val Tyr Gln Gly Glu Arg
 250 255 260
 gta aag att cag gaa aaa ttt aag aat gga atg cta cat ggt gat aaa 919
 Val Lys Ile Gln Glu Lys Phe Lys Asn Gly Met Leu His Gly Asp Lys
 265 270 275
 gtt tct ttc ttc tgc aaa aat aag gaa aag aag tgt agc tat aca gag 967
 Val Ser Phe Cys Lys Asn Lys Glu Lys Lys Cys Ser Tyr Thr Glu
 280 285 290
 gat gct cag tgt ata gat ggc act atc gaa gtc ccc aaa tgc ttc aag 1015
 Asp Ala Gln Cys Ile Asp Gly Thr Ile Glu Val Pro Lys Cys Phe Lys
 295 300 305
 gaa cac agt tct ctg gct ttt tgg aaa act gat gca tcc gat gta aag 1063
 Glu His Ser Ser Leu Ala Phe Trp Lys Thr Asp Ala Ser Asp Val Lys
 310 315 320 325
 cca tgc taagggtggtt ttacagattcc acataaaatg tcacacttgt ttcttggtca 1119
 Pro Cys
 tccaaggaac ctaattgaaa tttaaaaaata aagctactga atttattgcc gcaaaaaaaa 1179
 aaaaaaaa 1187

<210> 106

<211> 345

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> 1..19

<400> 106

Met Ile Ser Pro Val Leu Ile Leu Phe Ser Ser Phe Leu Cys His Val
 -15 -10 -5
 Ala Ile Ala Gly Arg Thr Cys Pro Lys Pro Asp Asp Leu Pro Phe Ser
 1 5 10
 Thr Val Val Pro Leu Lys Thr Phe Tyr Glu Pro Gly Glu Glu Ile Thr
 15 20 25
 Tyr Ser Cys Lys Pro Gly Tyr Val Ser Arg Gly Gly Met Arg Lys Phe
 30 35 40 45
 Ile Cys Pro Leu Thr Gly Leu Trp Leu Ile Asn Thr Leu Lys Cys Thr
 50 55 60
 Pro Arg Val Cys Pro Phe Ala Gly Ile Leu Glu Asn Gly Ala Val Arg
 65 70 75
 Tyr Thr Thr Phe Glu Tyr Pro Asn Thr Ile Ser Phe Ser Cys Asn Thr
 80 85 90
 Gly Phe Tyr Leu Asn Gly Ala Asp Ser Ala Lys Cys Thr Glu Glu Gly
 95 100 105
 Lys Trp Ser Pro Glu Leu Pro Val Cys Ala Pro Ile Ile Cys Pro Pro
 110 115 120 125
 Pro Ser Ile Pro Thr Phe Ala Thr Leu Arg Val Tyr Lys Pro Ser Ala
 130 135 140
 Gly Asn Asn Ser Leu Tyr Arg Asp Thr Ala Val Phe Glu Cys Leu Pro
 145 150 155
 Gln His Ala Met Phe Gly Asn Asp Thr Ile Thr Cys Thr Thr His Gly
 160 165 170
 Asn Trp Thr Lys Leu Pro Glu Cys Arg Glu Val Lys Cys Pro Phe Pro
 175 180 185
 Ser Arg Pro Asp Asn Gly Phe Val Asn Tyr Pro Ala Lys Pro Thr Leu
 190 195 200 205

Tyr Tyr Lys Asp Lys Ala Thr Phe Gly Cys His Asp Gly Tyr Ser Leu
 210 215 220
 Asp Gly Pro Glu Glu Ile Glu Cys Thr Lys Leu Gly Asn Trp Ser Ala
 225 230 235
 Met Pro Ser Cys Lys Ala Ser Cys Lys Val Pro Val Lys Lys Ala Thr
 240 245 250
 Val Val Tyr Gln Gly Glu Arg Val Lys Ile Gln Glu Lys Phe Lys Asn
 255 260 265
 Gly Met Leu His Gly Asp Lys Val Ser Phe Phe Cys Lys Asn Lys Glu
 270 275 280 285
 Lys Lys Cys Ser Tyr Thr Glu Asp Ala Gln Cys Ile Asp Gly Thr Ile
 290 295 300
 Glu Val Pro Lys Cys Phe Lys Glu His Ser Ser Leu Ala Phe Trp Lys
 305 310 315
 Thr Asp Ala Ser Asp Val Lys Pro Cys
 320 325

<210> 107
 <211> 1520
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..15

<220>
 <221> CDS
 <222> 16..1449

<220>
 <221> 3'UTR
 <222> 1450..1520

<220>
 <221> polyA_signal
 <222> 1483..1488

<220>
 <221> polyA_site
 <222> 1505..1520

<400> 107
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 Met Ala Ala Gly Gly Ser Gly Val Gly Gly Lys Arg
 1 5 10
 agc tcg aaa agc gat gcc gat tct ggt ttc ctg ggg ctg cgg ccc act 99
 Ser Ser Lys Ser Asp Ala Asp Ser Gly Phe Leu Gly Leu Arg Pro Thr
 15 20 25
 tcg gtg gac cca gcg ctg agg cgg cgg cgg cga ggc cca aga aat aag 147
 Ser Val Asp Pro Ala Leu Arg Arg Arg Arg Arg Arg Gly Pro Arg Asn Lys
 30 35 40
 aag cgg ggc tgg cgg cgg ctt gct cag gag cgg ctg ggg ctg gag gtt 195
 Lys Arg Gly Trp Arg Arg Leu Ala Gln Glu Pro Leu Gly Leu Glu Val
 45 50 55 60
 gac cag ttc ctg gaa gac gtg cgg cta cag gag cgc acg agc ggt ggc 243
 Asp Gln Phe Leu Glu Asp Val Arg Leu Gln Glu Arg Thr Ser Gly Gly
 65 70 75
 ttg ttg tca gag gcc cca aat gaa aaa ctc ttc ttc gtg gac act ggc 291
 Leu Leu Ser Glu Ala Pro Asn Glu Lys Leu Phe Phe Val Asp Thr Gly
 80 85 90
 tcc aag gaa aaa ggg ctg aca aag aag aga acc aaa gtc cag aag aag 339
 Ser Lys Glu Lys Gly Leu Thr Lys Lys Arg Thr Lys Val Gln Lys Lys

Phe Arg Leu Arg Gly Ile Lys Ala Gln Val Ala Leu Arg Leu Ala Glu
 370 375 380
 Leu Ala Arg Arg Gln Arg Arg Gln Ala Arg Glu Ala Glu Ala
 385 390 395 400
 Asp Lys Pro Arg Arg Leu Gly Arg Leu Lys Tyr Gln Ala Pro Asp Ile
 405 410 415
 Asp Val Gln Leu Ser Ser Glu Leu Thr Asp Ser Leu Arg Thr Leu Lys
 420 425 430
 Pro Glu Gly Asn Ile Leu Arg Asp Arg Phe Lys Ser Phe Gln Arg Arg
 435 440 445
 Asn Met Ile Glu Pro Arg Glu Arg Ala Lys Phe Lys Arg Lys Tyr Lys
 450 455 460
 Val Lys Leu Val Glu Lys Arg Ala Phe Arg Glu Ile Gln Leu
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 tctgcacagc ttctccgata ccaggtttc ataa atg tgt ttg ttg ctt tcc tgc 115
 Met Cys Leu Leu Ser Cys
 -10
 cct tgc cac ccc tct gcc cac gga cag tcc atg tgg att gag aga acc 163
 Pro Cys His Pro Ser Ala His Gly Gln Ser Met Trp Ile Glu Arg Thr
 -5 1 5
 tcc ttc gtg act gca tac aag ctg ccg ggg atc ctg cgc tgg ttt gag 211
 Ser Phe Val Thr Ala Tyr Lys Leu Pro Gly Ile Leu Arg Trp Phe Glu
 10 15 20 25
 gtg gtg cac atg tgc cag acc aca att agt cct ctg gag aat gcc ata 259
 Val Val His Met Ser Gln Thr Thr Ile Ser Pro Leu Glu Asn Ala Ile
 30 35 40
 gaa acc atg tcc acg gcc aat gag aag atc ctg atg atg ata aac cag 307
 Glu Thr Met Ser Thr Ala Asn Glu Lys Ile Leu Met Met Ile Asn Gln
 45 50 55
 tac cag agt gat gag acc ctc ccc atc aac cca ctc tcc atg ctc ctg 355
 Tyr Gln Ser Asp Glu Thr Leu Pro Ile Asn Pro Leu Ser Met Leu Leu
 60 65 70
 aac ggg att gtg gac cct gct gtc atg gga ggc ttc gcc aag tat gag 403
 Asn Gly Ile Val Asp Pro Ala Val Met Gly Gly Phe Ala Lys Tyr Glu
 75 80 85

aag Lys	gcc Ala	ttc Phe	ttc Phe	act Thr	gaa Glu	gag Tyr	tat Val	gtc Val	agg Arg	sac His	cac Pro	cct Glu	gag Asp	gac Gln	cag Gln	451
90					95				100						105	
gac Asp	aag Lys	ctg Leu	acc Thr	cac His	ctc Leu	aag Cys	gag Asp	ctg Val	att Leu	gca Trp	tgg Gln	cag Gln	atc Ser	ccc Asn	ttc Phe	499
				110					115					120		
leu Leu	gga Gly	gct Ala	ggg Gly	att Ile	aag Lys	cat Ile	gag His	aaa Glu	agg Lys	gtg Val	tca Ser	gat Asp	aac Asn	ttg Leu		547
				125				130					135			
cga Arg	ccc Pro	ttc Phe	tcc His	gac Asp	cgg Arg	atg Met	gag Glu	gaa Glu	tgt Cys	ttc Phe	aag Lys	aac Asn	atc Leu	aaa Lys	atg Met	595
				140				145					150			
aag Lys	gtg Val	gag Glu	aag Lys	gag Glu	tac Tyr	ggt Gly	gtt Val	cga Arg	atg Glu	met Glu	cct Pro	gac Asp	ttt Gln	gac Gln	gac Asp	643
				155		160					165					
agg Arg	aga Arg	gtg Val	ggc Gly	cgt Arg	ccc Pro	agg Ser	tct Ser	atg Met	ctg Leu	cgc Arg	tca Ser	tac Tyr	aga Arg	cag Gln	atg Met	691
				170		175				180				185		
tcc Ser	atc Ile	atc Ile	tct Ser	ctg Leu	gct Ala	tcc Ser	atg Met	aat Asn	tct Ser	gac Asp	tcg Cys	agc Ser	acc Thr	ccc Pro	agc Ser	739
				190					195					200		
aag Lys	cct Pro	acc Thr	tca Glu	gag Ser	agc Glu	ttt Gly	gac Ser	ctg Leu	gaa Leu	tta Ala	gca Ala	tca Ser	ccc Pro	aag Lys	acg Thr	787
				205				210					215			
ccg Pro	aga Arg	gtg Val	cag Glu	gag Gln	gag Glu	gaa Glu	ccg Pro	atc Ile	tcc Ser	ccg Pro	ggg Gly	agc Ser	acc Thr	ctg Leu	cct Pro	835
				220		225							230			
gag Glu	gtc Val	ctg Lys	ctg Leu	cgg Arg	agg Arg	tcc Ser	aag Lys	aag Lys	agg Arg	aca Thr	aag Lys	aga Arg	agc Ser	agc Ser	gta Val	883
				235		240					245					
gtt Val	ttt Phe	cgq Ala	gat Ser	gag Glu	gag Glu	aaa Gly	gca Ala	gct Ala	gca Glu	tcg Glu	gac Ser	ctg Asp	aug Lys	cgg Arg	ctt Leu	931
				250		255				260				265		
tcc Ser	agg Arg	aag Lys	cat His	gag Glu	gtc Phe	atg Met	agt Ser	gac Asp	acc Thr	aat Asn	ctc Leu	ctg Ser	gla Glu	cat His	gcg Ala	979
				270					275					280		
gcc Ala	atc Ile	ccc Pro	ctc Leu	aac Lys	gcg Ala	tct Ser	gtc Val	ctc Ser	tct Ser	caa Gln	atg Met	agc Ser	ttt Ser	gcc Phe	agc Ser	1027
				285				290					295			
cag Gln	ctc Ser	atc Met	cct Pro	acc Thr	acc Ile	cca Gly	gcc Ala	ctg Ala	gcg Leu	ctc Ala	tca Ser	gtg Val	gca Ala	ggc Gly	ile Ile	1075
				300		305						310				
cct Pro	ggg Gly	ttg Leu	gat Asp	gag Glu	gcc Ala	aac Asn	aca Thr	tct Ser	ccc Ser	cgc Arg	ctc Leu	agc Ser	cag Gln	acc Thr	ttc Phe	1123
				315		320					325					
ctc Leu	caa Gln	ctc Leu	tca Ser	gat Asp	ggt Gly	gac Gly	aag Lys	aag Lys	aca Thr	ctc Thr	aca Thr	cgg Arg	aag Lys	aag Lys	gtc Val	1171
				330		335				340						

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 <213> Homo sapiens

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 <221> SIGNAL
 <222> 1..15

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 5 10 15
 Gly Ile Leu Arg Trp Phe Glu Val Val His Met Ser Gln Thr Thr Ile
 20 25 30
 Ser Pro Leu Glu Asn Ala Ile Glu Thr Met Ser Thr Ala Asn Glu Lys
 35 40 45
 Ile Leu Met Met Ile Asn Gln Tyr Gln Ser Asp Glu Thr Leu Pro Ile
 50 55 60 65
 Asn Pro Leu Ser Met Leu Leu Asn Gly Ile Val Asp Pro Ala Val Met
 70 75 80
 Gly Gly Phe Ala Lys Tyr Glu Lys Ala Phe Phe Thr Glu Glu Tyr Val
 85 90 95
 Arg Asp His Pro Glu Asp Gln Asp Lys Leu Thr His Leu Lys Asp Leu
 100 105 110
 Ile Ala Trp Gln Ile Pro Phe Leu Gly Ala Gly Ile Lys Ile His Glu
 115 120 125
 Lys Arg Val Ser Asp Asn Leu Arg Pro Phe His Asp Arg Met Glu Glu
 130 135 140 145
 Cys Phe Lys Asn Leu Lys Met Lys Val Glu Lys Glu Tyr Gly Val Arg
 150 155 160
 Glu Met Pro Asp Phe Asp Asp Arg Arg Val Gly Arg Pro Arg Ser Met
 165 170 175
 Leu Arg Ser Tyr Arg Gln Met Ser Ile Ile Ser Leu Ala Ser Met Asn
 180 185 190
 Ser Asp Cys Ser Thr Pro Ser Lys Pro Thr Ser Glu Ser Phe Asp Leu
 195 200 205
 Glu Leu Ala Ser Pro Lys Thr Pro Arg Val Glu Gln Glu Pro Ile
 210 215 220 225
 Ser Pro Gly Ser Thr Leu Pro Glu Val Lys Leu Arg Arg Ser Lys Lys
 230 235 240
 Arg Thr Lys Arg Ser Ser Val Val Phe Ala Asp Glu Lys Ala Ala Ala
 245 250 255
 Glu Ser Asp Leu Lys Arg Leu Ser Arg Lys His Glu Phe Met Ser Asp
 260 265 270
 Thr Asn Leu Ser Glu His Ala Ala Ile Pro Leu Lys Ala Ser Val Leu
 275 280 285
 Ser Gln Met Ser Phe Ala Ser Gln Ser Met Pro Thr Ile Pro Ala Leu
 290 295 300 305
 Ala Leu Ser Val Ala Gly Ile Pro Gly Leu Asp Glu Ala Asn Thr Ser
 310 315 320
 Pro Arg Leu Ser Gln Thr Phe Leu Gln Leu Ser Asp Gly Asp Lys Lys
 325 330 335
 Thr Leu Thr Arg Lys Lys Val Asn Gln Phe Phe Lys Thr Met Leu Ala
 340 345 350
 Ser Lys Ser Ala Glu Glu Gly Lys Gln Ile Pro Asp Ser Leu Ser Thr
 355 360 365
 Asp Leu
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 tcactggccc tgatcacttg aagggtgcagc aagtcactga ga atg agc act ttc 114
 Met Ser Thr Phe
 1
 ttc tcg gac aca gca tgg atc tgc ctg gct gtc ccc aca gta cta tgt 162
 Phe Ser Asp Thr Ala Trp Ile Cys Leu Ala Val Pro Thr Val Leu Cys
 5 10 15 20
 ggg aca gta ttt tgc aaa tac aag aag agc tca ggg cag ctg tgg agc 210
 Gly Thr Val Phe Cys Lys Tyr Lys Lys Ser Ser Gly Gln Leu Trp Ser
 25 30 35
 tgg atg gtc tgc ctg gca ggc ctc tgt gca gtc tgc ctg ctc atc ctg 258
 Trp Met Val Cys Leu Ala Gly Leu Cys Ala Val Cys Leu Leu Ile Leu
 40 45 50
 tcc cct ttt tgg ggc ttg atc ctc ttc tcg gtg tca tgc ttc ctc atg 306
 Ser Pro Phe Trp Gly Leu Ile Leu Phe Ser Val Ser Cys Phe Leu Met
 55 60 65
 tat act tac tta tct ggc caa gaa ttg tta cct gtg gat cag aag gca 354
 Tyr Thr Tyr Leu Ser Gly Gln Glu Leu Leu Pro Val Asp Gln Lys Ala
 70 75 80
 gtc ctg gtg aca ggt ggt gat tgc ggg ctt ggc cat gct ttg tgc aag 402
 Val Leu Val Thr Gly Gly Asp Cys Gly Leu Gly His Ala Leu Cys Lys
 85 90 95 100
 tat ctg gat gag ctg ggc ttc acg gta ttt gcc gga gtt ttg aat gaa 450
 Tyr Leu Asp Glu Leu Gly Phe Thr Val Phe Ala Gly Val Leu Asn Glu
 105 110 115
 aat ggc cca gga gct gag gaa ttg cga aga acc tgc tct ccg cgc ctc 498
 Asn Gly Pro Gly Ala Glu Glu Leu Arg Arg Thr Cys Ser Pro Arg Leu
 120 125 130
 tcg gtg ctc caa atg gac atc acg aag cca gtg cag ata aaa gat gct 546
 Ser Val Leu Gln Met Asp Ile Thr Lys Pro Val Gln Ile Lys Asp Ala
 135 140 145
 tac agc aag gtt gca gca atg ctg cag gac aga gga ctg tgg gct gtg 594
 Tyr Ser Lys Val Ala Ala Met Leu Gln Asp Arg Gly Leu Trp Ala Val
 150 155 160
 atc aac aat gct ggg gtg ctt ggc ttt cca act gat ggg gag ctt ctt 642
 Ile Asn Asn Ala Gly Val Leu Gly Phe Pro Thr Asp Gly Glu Leu Leu
 165 170 175 180
 ctt atg act gac tac aaa caa tgc atg gcc gtg aac ttc ttt gga act 690

115	120	125
Ser Pro Arg Leu Ser Val	Leu Gln Met Asp Ile Thr Lys	Pro Val Gln
130	135	140
Ile Lys Asp Ala Tyr Ser	Lys Val Ala Ala Met Leu	Gln Asp Arg Gly
145	150	155
Leu Trp Ala Val Ile Asn	Asn Ala Gly Val Leu	Gly Phe Pro Thr Asp
165	170	175
Gly Glu Leu Leu Met Thr	Asp Tyr Lys Gln Cys Met	Ala Val Asn
180	185	190
Phe Phe Gly Thr Val Glu	Val Thr Lys Thr Phe Leu	Pro Leu Leu Arg
195	200	205
Lys Ser Lys Gly Arg Leu	Val Asn Val Ser Ser Met	Gly Gly Gly Ala
210	215	220
Pro Val Glu Arg Leu Ala	Ser Tyr Gly Ser Ser Lys	Ala Ala Val Thr
225	230	235
Met Phe Ser Ser Val Met	Arg Leu Glu Leu Ser Lys	Trp Gly Ile Lys
245	250	255
Val Ala Ser Ile Gln Pro	Gly Gly Phe Leu Thr Asn	Ile Ala Gly Thr
260	265	270
Ser Asp Lys Trp Glu Lys	Leu Glu Lys Asp Ile Leu	Asp His Leu Pro
275	280	285
Ala Glu Val Gln Glu Asp	Tyr Cys Gln Asp Tyr Ile	Leu Ala Gln Arg
290	295	300
Asn Phe Leu Leu Leu Ile	Asn Ser Leu Ala Ser Lys	Asp Phe Ser Pro
305	310	315
Val Leu Arg Asp Ile Gln	His Ala Ile Leu Ala Lys	Ser Pro Phe Ala
325	330	335
Tyr Tyr Thr Pro Gly Lys	Gly Ala Tyr Leu Trp Ile	Cys Leu Ala His
340	345	350
Tyr Leu Pro Ile Gly Ile	Tyr Asp Tyr Phe Ala Lys	Arg His Phe Gly
355	360	365
Gln Asp Lys Pro Met Pro	Arg Ala Leu Arg Met Pro	Asn Tyr Lys Lys
370	375	380
Lys Ala Pro		
385		